

# Sequence Listing

- <110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Smith, Victoria  
Stewart, Timothy A.  
Tumas, Daniel  
Watanabe, Colin K.  
Williams, P. Mickey  
Wood, William I.
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<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
     1                    5                    10                    15  
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
                     20                    25                    30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro  
                     35                    40                    45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
                     50                    55                    60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
                     65                    70                    75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
                     80                    85                    90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
                     95                    100                    105

Asp	His	Trp	Lys	Ala 110	Leu	Ala	Phe	Arg	Leu 115	Glu	Glu	Glu	Gln	Lys 120
Met	Arg	Pro	Glu	Ile 125	Ala	Gly	Leu	Lys	Pro 130	Ala	Asn	Pro	Pro	Val 135
Leu	Pro	Ala	Pro	Gln 140	Lys	Ala	Asp	Thr	Asp 145	Pro	Glu	Asn	Leu	Pro 150
Glu	Ile	Ser	Ser	Gln 155	Lys	Thr	Gln	Arg	His 160	Ile	Gln	Arg	Gly	Pro 165
Pro	His	Leu	Gln	Ile 170	Arg	Pro	Pro	Ser	Gln 175	Asp	Leu	Lys	Asp	Gly 180
Thr	Gln	Glu	Glu	Ala 185	Thr	Lys	Arg	Gln	Glu 190	Ala	Pro	Val	Asp	Pro 195
Arg	Pro	Glu	Gly	Asp 200	Pro	Gln	Arg	Thr	Val 205	Ile	Ser	Trp	Arg	Gly 210
Ala	Val	Ile	Glu	Pro 215	Glu	Gln	Gly	Thr	Glu 220	Leu	Pro	Ser	Arg	Arg 225
Ala	Glu	Val	Pro	Thr 230	Lys	Pro	Pro	Leu	Pro 235	Pro	Ala	Arg	Thr	Gln 240
Gly	Thr	Pro	Val	His 245	Leu	Asn	Tyr	Arg	Gln 250	Lys	Gly	Val	Ile	Asp 255
Val	Phe	Leu	His	Ala 260	Trp	Lys	Gly	Tyr	Arg 265	Lys	Phe	Ala	Trp	Gly 270
His	Asp	Glu	Leu	Lys 275	Pro	Val	Ser	Arg	Ser 280	Phe	Ser	Glu	Trp	Phe 285
Gly	Leu	Gly	Leu	Thr 290	Leu	Ile	Asp	Ala	Leu 295	Asp	Thr	Met	Trp	Ile 300
Leu	Gly	Leu	Arg	Lys 305	Glu	Phe	Glu	Glu	Ala 310	Arg	Lys	Trp	Val	Ser 315
Lys	Lys	Leu	His	Phe 320	Glu	Lys	Asp	Val	Asp 325	Val	Asn	Leu	Phe	Glu 330
Ser	Thr	Ile	Arg	Ile 335	Leu	Gly	Gly	Leu	Leu 340	Ser	Ala	Tyr	His	Leu 345
Ser	Gly	Asp	Ser	Leu 350	Phe	Leu	Arg	Lys	Ala 355	Glu	Asp	Phe	Gly	Asn 360
Arg	Leu	Met	Pro	Ala 365	Phe	Arg	Thr	Pro	Ser 370	Lys	Ile	Pro	Tyr	Ser 375
Asp	Val	Asn	Ile	Gly 380	Thr	Gly	Val	Ala	His 385	Pro	Pro	Arg	Trp	Thr 390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe



His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgctg aggcccgga ggccgggccg gccgggctgc gagcgctgc 50  
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ccctcggaag tgttcgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcggggccctc cccgtgcctg 300  
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
 cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400  
 ctggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450  
 gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500  
 cagcgctcat caacgtgggc ttcctggaga gcagcaacag cacggactac 550  
 attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
 tggctttcct gaggctgggc ccttcacgt ggctccccg gagctccacc 650  
 ctctctacca ctacaagacc tatgtcggcg gcctcctgct gctctccaag 700  
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 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800  
 ttttcgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850  
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 accatgtggc ttccgcact gccctgtctg tgggcggggc cccctgcaact 1000  
 gtctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050  
 attcagctga gctggatgga cagtaggaa gcctgtacct acaggccata 1100  
 ttgtcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150  
 atgtggagt gccaggacca agacagcaag ctacgcaatt gcagccacc 1200  
 ggccgccaag gcaggcttg gctgggccag gacacgtggg gtgcctggga 1250  
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 cgggacccc cctgccttcc tgctaccct actctgacct ccttcacgtg 1350  
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450  
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens  
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<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.  
  
 <220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.  
  
 <220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.  
  
 <220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.  
  
 <220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp  
   1                  5                  10                  15  
  
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
                   20                  25                  30  
  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                   35                  40                  45  
  
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
                   50                  55                  60  
  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
                   65                  70                  75  
  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
                   80                  85                  90  
  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
                   95                  100                  105  
  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
                   110                  115                  120  
  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
                   125                  130                  135  
  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

	140		145		150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp				
155	160				165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala				
170	175				180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His				
185	190				195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His				
200	205				210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly				
215	220				225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu				
230	235				240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe				
245	250				255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg				
260	265				270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly				
275	280				285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu				
290	295				300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp				
305	310				315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser				
320	325				

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
 gcgaacgctt cgaggagtcc tgg 23

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-24  
<223> Synthetic construct

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
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gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18



<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ggctccgggg cggcccgtta ggccagtgcg ccgcgcgctc ccccgcaggc 200

cccggcccgc agcatggagc caccggagc ccggcggggc cgcgcgcagc 250

cgccgctggt gctgccgctc tcgctgttag cgctgctgc gctgctggga 300

ggcggcgggc gcggcggggc cgcggcgctg cccgccggct gcaagcacga 350

tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400

tgggtgtgcag cagcctggaa ctgcgcagg tcctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500

gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550

gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600

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acatgtgaaa aaatatttatt tgacttaaaa gtttatttat ttgttttttt 2350  
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<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
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 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
 20 25 30  
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90





<223> Synthetic construct

<400> 25

gaggactcac caatctgggt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accagggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctgggtgctg 50

ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtctt ttgggagaac agattatatt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

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[illegible]

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<220>
<221> sig_peptide
<222> 1-21
<223> Signal peptide.
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<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens
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35

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accttcttct cctgcacgc gtgtgtggct tacgccaccg aagtggcctg 600  
gacccggggc cgcccgccg agatcactgg ctatatggcc accgtaccgc 650  
ggctgctgaa ggtgctggag accttcgttg cctgcacat cttcgcgttc 700  
atcagcgacc ccaacctgta ccagcaccag ccggccctgg agtgggtgcgt 750  
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ctggccccct taccagttcg atgagaagta tggcggccag cctcggcgct 950  
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tgtggctgac ctgggtgact ctgccacct ggtttttgtc aaggtctaag 1100  
actctcccaa gaggetcccg ttccctctcc aacctcttg ttcttcttgc 1150  
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Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	215	220	225
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	230	235	240
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	245	250	255
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	260	265	270
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	275	280	285
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	290	295	300
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	305	310	315
His	Leu	Val	Phe	Val	Lys	Val									320		

<210> 32  
 <211> 3680  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 tcacctcggc ctcccaaagt gctgggatta caggcatgag ccaactgacgc 150  
 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200  
 taaacattgg gcactacagt gacccaaaaca gactgaattc cccaagagcc 250  
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
 ttattactca ctatgactaa gggtcacaaa tgggggtacgt tgatggagag 350  
 tgatttggtta agagactaca gagggaggac agactaccaa gagggggggcc 400  
 aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450  
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500  
 cactcactac actttggcct gagaaaatag catgggattg gagggaggctg 550  
 ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600  
 aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650  
 gcagggtgaa tcattaggtc ttatcaacag atatgggcaa gcaagccag 700



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 cacaggggtg gccgggagtt gtcagctgat gcctgctgag aggcaggaat 3300  
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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
			20						25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
			35						40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
			50						55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
			65						70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
			80						85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
			95						100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
			110						115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
			125						130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
			140						145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
			155						160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
			170						175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
			185						190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
			200						205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
			215						220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
			230						235					240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
			335											

<210> 34  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct

<400> 34  
 tgtcctttgt ccagacttc tgtcc 25

<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 35  
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggg cgctctgtta cacaagcaag atacagccag cccacctaa 50

ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cacacttaac 100

ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150

tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200

tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250

caatctattc ttgccacatc aagggattgt tttccttta aaaaaaacc 300

aataccaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350  
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaactc aaggcgagtc attcccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650  
ccttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcccat ctcagcacat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850  
ccatctgtga ccccttgat agtggaaacca agtggatggc ttaccacaaa 900  
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gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050  
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agaaatgaac cagttctgcy attagacaat gcaccggaac cttatgatgt 1200  
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250  
tgccagaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300  
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gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000  
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ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
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Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330
Arg Thr Ser Val														

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 aacaggatct cctcttcgag tctgcagccc aggacgctga ttccagcagc 50  
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 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150  
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
 tgccaccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
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 tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350  
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ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600  
 aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650  
 aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700  
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 ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800  
 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
 agaagtcaga gatttacaat atgactttta cattaagggt tatgggatac 950  
 tcaagatatt tactcatgca tttactctat tgcttatgct ttaaaaaaag 1000  
 gaaaaaaaaaaa aaactacta accactgcaa gctcttgtca aatttttagtt 1050  
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 ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
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 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
 tgtgtaggtg ctgaatgctg taaggagttt aggttgtagt aattctacaa 1550  
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
1				5					10					15

Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 45  
 gggaactgct atctgatgcc 20

<210> 46  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 46  
 caggatctcc tcttgagtc tgcagc 26

<210> 47  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 47  
 cttctcgaac cacataagtt tgaggcag 28

<210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 48  
 cacgattccc tccacagcaa ctggg 25

<210> 49  
 <211> 1969  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50



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 gatcagggttg aatgaatgga actcttctctg tctggcctcc aaagcagcct 1600  
 agaagctgag gggctgtggt tgaggggacc tccaccctgg ggaagtccga 1650  
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggcccctgg 1700  
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
 gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800  
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
 attccggcct gaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950  
 aaaaaaaaaa aaaaaaaga 1969

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu  
 20 25 30  
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45  
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60  
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
 80 85 90  
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
 95 100 105  
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
 110 115 120  
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
 125 130 135  
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
 140 145 150  
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
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Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
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 <212> DNA  
 <213> Homo sapiens

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 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

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Gly	Ala	Ala	Gly	Ser	Lys	Val	Ser	Glu	Ala	Leu	Gly	Gln	Gly	Thr
				65					70					75
Arg	Glu	Ala	Val	Gly	Thr	Gly	Val	Arg	Gln	Val	Pro	Gly	Phe	Gly
				80					85					90
Ala	Ala	Asp	Ala	Leu	Gly	Asn	Arg	Val	Gly	Glu	Ala	Ala	His	Ala
				95					100					105
Leu	Gly	Asn	Thr	Gly	His	Glu	Ile	Gly	Arg	Gln	Ala	Glu	Asp	Val
				110					115					120
Ile	Arg	His	Gly	Ala	Asp	Ala	Val	Arg	Gly	Ser	Trp	Gln	Gly	Val
				125					130					135
Pro	Gly	His	Ser	Gly	Ala	Trp	Glu	Thr	Ser	Gly	Gly	His	Gly	Ile
				140					145					150
Phe	Gly	Ser	Gln	Gly	Gly	Leu	Gly	Gly	Gln	Gly	Gln	Gly	Asn	Pro
				155					160					165
Gly	Gly	Leu	Gly	Thr	Pro	Trp	Val	His	Gly	Tyr	Pro	Gly	Asn	Ser
				170					175					180
Ala	Gly	Ser	Phe	Gly	Met	Asn	Pro	Gln	Gly	Ala	Pro	Trp	Gly	Gln
				185					190					195
Gly	Gly	Asn	Gly	Gly	Pro	Pro	Asn	Phe	Gly	Thr	Asn	Thr	Gln	Gly
				200					205					210
Ala	Val	Ala	Gln	Pro	Gly	Tyr	Gly	Ser	Val	Arg	Ala	Ser	Asn	Gln
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Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly
				230					235					240
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser
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Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly
				305					310					315
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His
				320					325					330
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly
				335					340					345

Glu Ser Gly Ile	Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser	Asn
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Met Arg Glu Ile	Ser Lys Glu Gly Asn	Arg Leu Leu Gly Gly	Ser
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Gly Asp Asn Tyr	Arg Gly Gln Gly Ser	Ser Trp Gly Ser Gly	Gly
380	385		390
Gly Asp Ala Val	Gly Gly Val Asn Thr	Val Asn Ser Glu Thr	Ser
395	400		405
Pro Gly Met Phe	Asn Phe Asp Thr Phe	Trp Lys Asn Phe Lys	Ser
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Lys Leu Gly Phe	Ile Asn Trp Asp Ala	Ile Asn Lys Asp Gln	Arg
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Ser Ser Arg Ile	Pro		
440			

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 <211> 3580  
 <212> DNA  
 <213> Homo sapiens

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
				35					40					45
His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
				50					55					60
Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
				110					115					120
Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
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Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
				140					145					150
Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
				155					160					165
Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
				170					175					180
Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
				185					190					195
Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
				200					205					210
Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245					250					255
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
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<212> DNA  
<213> Homo sapiens

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<210> 56  
<211> 299  
<212> PRT  
<213> Homo sapiens

<400> 56  
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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
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Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr			290	295	

<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

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cagtggaatc ccacccccac gggtcacctg ggccaaggat gggccagtg 1150  
tcaccggcta caacaagacg cgcttctgc tgagcaacct cctcatcgac 1200  
accaccagcg aggaggactc aggcacctac cgctgcatgg ccgacaatgg 1250  
ggttgggcag cccggggcag cggtcacact ctacaatgtc caggtgtttg 1300  
aaccctctga ggtcaccatg gagctatccc agctgggtcat cccctggggc 1350  
cagagtgcca agcttacctg tgaggtgcgt gggaaacccc cgccctccgt 1400  
gctgtggctg aggaatgctg tgccctcat ctccagccag cgcctccggc 1450





<212> PRT

<213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu	
1				5					10					15	
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	
				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr	Gln
	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val	Gln
	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln	Asp
	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys	Leu
	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro	Arg
	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly	Glu
	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser	Ser
	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg	Pro
	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val	Val
	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr	Ile
	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg	Leu
	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn	Cys
	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly	Arg



Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
				950					955					960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
				965					970					975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	
				980					985					990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	
				995					1000					1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
				1010					1015					1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	
				1025					1030					1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	
				1040					1045					1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
				1055					1060					1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	
				1070					1075					1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	
				1085					1090					1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	
				1100					1105					1110	
Pro	Pro	Leu	Thr	Ile											
				1115											

<210> 59  
 <211> 25  
 <212> DNA  
 <213> Artificial



<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 59  
gggaaacaca gcagtcattg cctgc 25

<210> 60  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 60  
gcacacgtag cctgtcgctg gagc 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-42  
<223> Synthetic construct.

<400> 61  
caccctaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
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cgcctgctcc tcccaggctc ccgcggccga cccccgcgca acatgcagcc 100  
cacgggccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcgctc 150  
tgctgctcct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgcg 200  
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250  
cctcttcacc acgccgggtg tccccagcgc cctcaactacc ccaggcctca 300  
ctacgccagg caccctgacc accctggacc ttccggggctg cgcgcaggcc 350



<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

	260	265	270
Ser Asp Thr Leu	Ile Arg Arg Val Leu	Glu Val Ser Gln Ala	Pro
	275	280	285
Val Ile Phe Ser	His Ser Ala Ala Arg	Ala Val Cys Asp Asn	Leu
	290	295	300
Leu Asn Val Pro	Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly	Gly
	305	310	315
Ile Val Met Val	Thr Leu Ser Met Gly	Val Leu Gln Cys Asn	Leu
	320	325	330
Leu Ala Asn Val	Ser Thr Val Ala Asp	His Phe Asp His Ile	Arg
	335	340	345
Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr	Asp
	350	355	360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr	Tyr
	365	370	375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu	Glu
	380	385	390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe	Arg
	395	400	405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro	Val
	410	415	420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His	Ser
	425	430	435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu	Val
	440	445	450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn	Ala
	455	460	465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile	Pro
	470	475	480
Thr Phe Thr Gln	Trp Leu Cys		
	485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcaccogag agcaggagct gaaagcctct 50

aacaccaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100

ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150

cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200

tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

tacaaccaga atgtatcca gaaggactgc aactgcctgc acgtggtgga 300

gcccatgcca gtgcctggcc atgacgtgga ggccactgc ctgctgtgcg 350

agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400

atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450

gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550

tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650  
atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850  
aagagggatg tgggtctctga tctctgttgt cttcttgggg ctttgggggt 900  
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttggaat gttgttacc ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100  
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ctctgctgcc ggtcccctca cctgcacttg aggggtcttg gcagtccctc 1350  
ctctccccag tgtccacagt cactgagcca gacggctcgg ttggaacatga 1400  
gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450  
gcctcttgtc cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500  
tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaattg 1550  
ttttatttct ctca 1564

<210> 68  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
1 5 10 15  
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
20 25 30  
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45  
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	65	70	75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	80	85	90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	95	100	105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	110	115	120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	125	130	135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	140	145	150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	155	160	165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	170	175	180

Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggtcctccc 150  
 tccctttgca ttccacccc tccgggcttt gcgctttcct ggggaccccc 200  
 tcgcccggag atggccgctg tgatgcggag caaggattcg tctgtctgcc 250  
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
 tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350  
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550  
 gcatgtgtcg cccagtagc cgctgcaata atggcatctg tatccagtt 600  
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650





aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150  
 tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200  
 tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
 tgctgagatc ctcaaataat ctcaatttca ggagggttca caaaatgtac 2300  
 tcctgaagta gacagagtag tgagggttca ttgccctcta taagcttctg 2350  
 actagccaat ggcatcatcc aattttcttc ccaaacctct gcagcatctg 2400  
 ctttattgcc aaagggctag tttcggtttt ctgcagccat tgcggttaaa 2450  
 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
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 aactcagttc taaatacttt gtctggagca caaaacaata aaagggtatc 2600  
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 atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950  
 gtccaccctt ttaaaaatta ttatttgaag taatttatat acaggaaatg 3000  
 ttaatgagat gtattttctt atagagatat ttottacaga aagctttgta 3050  
 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
 taagataaaa tctattaaat ttttctcttc taaaaactga aaaaaaaaaa 3150  
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
 65 70 75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
 80 85 90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
 95 100 105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
 110 115 120  
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
 155 160 165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
 170 175 180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
 200 205 210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 230 235 240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
 245 250 255  
 Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
 tctcaatctg ctgacctg gatccgcctg accttgtaat ccacctacct 50  
 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100  
 acatcacgtt tttaaaaatt gatttottca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200





Ser Ser Glu Asn	Ser Asn Gln Ile Pro	Ile Ser Leu Tyr Ser	Lys
230	235		240
Ser Leu Ser Glu	Pro Leu Asn Thr Ser	Leu Ser Met Thr Ser	Ala
245	250		255
Val Gln Asn Ser	Thr Tyr Thr Thr Ser	Val Ile Thr Ser Cys	Ser
260	265		270
Leu Thr Ser Ser	Ser Leu Asn Ser Ala	Ser Pro Val Ala Met	Ser
275	280		285
Ser Ser Tyr Asp	Gln Ser Ser Val His	Asn Arg Ile Pro Tyr	Gln
290	295		300
Ser Pro Val Ser	Ser Ser Glu Ser Ala	Pro Gly Thr Ile Met	Asn
305	310		315
Gly His Gly Gly	Gly Arg Ser Gln Gln	Thr Leu Asp Ser Lys	Tyr
320	325		330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu	Val Pro Thr Lys Gln	Arg
335	340		345
Lys Arg Ile Ala	His Val Met Trp Lys	Thr Pro Val Gly Gln	Trp
350	355		360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 74  
 tggtaaactg gcccaaactc gg 22

<210> 75  
 <211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
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ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100  
tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200  
caccgacggc ccccgccca ccccgcccta ctgggacggc gagaaggagg 250  
tgctggcggg ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350  
ctgggaccgg cagccgcccg gggccccca cgaccgcgcg gaccgcctgc 400  
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cgcgaccgcg tggctgtggg cgcggatgcc tttagcgcg gtgacttctc 500  
actgcgtatc gagccgttg aggtcgccga cgagggcacc tactcctgcc 550  
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gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750  
cagcagctgg gctacgtgct ggccacgctg ctgctcttca tctgtctact 800  
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ttcgctgtgg ctgcaggga ccagatgctt tacaggagtg aggacatcca 950  
gctagattac aaaaacaaca tctgaagga gagggcggag ctggcccaca 1000  
gcccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050



Ala Arg Gly Ala	Pro	Ala Leu Leu Thr	Cys	Val Asn Arg Gly	His
	80		85		90
Val Trp Thr Asp	Arg	His Val Glu Glu	Ala Gln Gln Val	Val	His
	95		100		105
Trp Asp Arg Gln	Pro	Pro Gly Val Pro	His Asp Arg Ala	Asp	Arg
	110		115		120
Leu Leu Asp Leu	Tyr	Ala Ser Gly Glu	Arg Arg Ala Tyr	Gly	Pro
	125		130		135
Leu Phe Leu Arg	Asp	Arg Val Ala Val	Gly Ala Asp Ala	Phe	Glu
	140		145		150
Arg Gly Asp Phe	Ser	Leu Arg Ile Glu	Pro Leu Glu Val	Ala	Asp
	155		160		165
Glu Gly Thr Tyr	Ser	Cys His Leu His	His His Tyr Cys	Gly	Leu
	170		175		180
His Glu Arg Arg	Val	Phe His Leu Thr	Val Ala Glu Pro	His	Ala
	185		190		195
Glu Pro Pro Pro	Arg	Gly Ser Pro Gly	Asn Gly Ser Ser	His	Ser
	200		205		210
Gly Ala Pro Gly	Pro	Asp Pro Thr Leu	Ala Arg Gly His	Asn	Val
	215		220		225
Ile Asn Val Ile	Val	Pro Glu Ser Arg	Ala His Phe Phe	Gln	Gln
	230		235		240
Leu Gly Tyr Val	Leu	Ala Thr Leu Leu	Leu Phe Ile Leu	Leu	Leu
	245		250		255
Val Thr Val Leu	Leu	Ala Ala Arg Arg	Arg Arg Gly Gly	Tyr	Glu
	260		265		270
Tyr Ser Asp Gln	Lys	Ser Gly Lys Ser	Lys Gly Lys Asp	Val	Asn
	275		280		285
Leu Ala Glu Phe	Ala	Val Ala Ala Gly	Asp Gln Met Leu	Tyr	Arg
	290		295		300
Ser Glu Asp Ile	Gln	Leu Asp Tyr Lys	Asn Asn Ile Leu	Lys	Glu
	305		310		315
Arg Ala Glu Leu	Ala	His Ser Pro Leu	Pro Ala Lys Tyr	Ile	Asp
	320		325		330
Leu Asp Lys Gly	Phe	Arg Lys Glu Asn	Cys Lys		
	335		340		

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens



<400> 78

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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atctttttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250  
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ccaccgggga ggacctgag ggctcagaca tcctgaacta ctttgagagc 350  
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gacacttctt cctggaccgc tgggtttttt gcgggtcacca ttgtctgcat 550  
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gccatgggag ggacggtcag cggcgtggcc tcattggtgg acttggctgc 700  
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aactttgctg acctatgtgg ccggcagctc accgcctgga tccagggtgc 1150  
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agattgtgcc cagggagctg gctgaggcca cgggagtggt gatgtccttt 1400  
tatgtgtgct tgggcttaac actgggctca gcctgtctta cctcctggt 1450



Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser			
	410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu			
	425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly			
	440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser			
	455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile			
	470	475	

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 80  
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<210> 81  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 81  
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<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 82  
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<210> 83  
 <211> 1844

<212> DNA  
<213> Homo sapiens

<400> 83

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cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcggttcg 1300  
ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350



Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
 cccctcgcga gggctctgaat ttctctgtgc tgttcacaaa gatgcttttt 250  
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 cctgacattt ggagctgcc tcttcttggt gctgatcacc agacctcaac 350  
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400  
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450  
 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgtg 500  
 tgtctgacaa tgggccctgc ttgggatata gaaaacaaa ccagccctac 550  
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 tctttgctca gaataggcca gagggatca tctccgaatt ggcttggttac 700  
 acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750



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agaagacttg cagaaaattg ggaaagaaaag tggccttaaa acttttgaac 2150  
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Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr			



Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

<210> 87  
 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

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 ccaggacatt ggtgaccgc caatccggtg tggacgactg gaagcccagc 150  
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200  
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<210> 90

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 90

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<210> 91

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 91

cccaggcaga gatgcagtac aggc 24

<210> 92

<211> 26

<212> DNA

<213> Artificial

<220>

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<222> 1-26

<223> Synthetic construct.

<400> 92

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<210> 93

<211> 47

<212> DNA

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<220>

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<222> 1-47

<223> Synthetic construct.

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<210> 94

<211> 3037

<212> DNA

<213> Homo sapiens

<400> 94

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aatgaaatag tgattatgaa aatacagtg tctgtaatta agctatgtct 1450





	230		235		240
Asn Ala Thr Gly	Val Ala Met Leu Phe	Ser Ala Gly Thr Phe	Leu		
	245		250		255
Tyr Val Ala Thr	Val His Val Leu Pro	Glu Val Gly Gly Ile	Gly		
	260		265		270
His Ser His Lys	Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser	Arg		
	275		280		285
Leu Glu Val Ala	Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu	Ile		
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Leu Ser Val Gly	His Gln His				
	305				

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 <213> Artificial

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 <223> Synthetic construct.

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<210> 97  
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 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 97  
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<210> 98  
 <211> 50  
 <212> DNA  
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<220>  
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 <223> Synthetic construct.

<400> 98  
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<210> 99  
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<212> DNA  
<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240



Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101  
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 <212> DNA  
 <213> Homo sapiens

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Ala Tyr Ala Gly	Leu 500	Leu Gly Thr Ile	Glu 505	Leu Lys Leu Asp	Leu 510
Val Leu Leu Gly	Ala 515	Val Ala Ala Val	Ser 520	Ser Phe Leu Pro	Phe 525
Leu Trp Lys Ala	Trp 530	Ala Gly Trp Gly	Ser 535	Lys Arg Pro Leu	Ala 540
Thr Leu Phe Pro	Ile 545	Pro Gly Pro Val	Leu 550	Leu Leu Leu Leu	Phe 555
Arg Leu Ala Val	Phe 560	Phe Ser Asp Ser	Phe 565	Val Val Ala Glu	Ala 570
Arg Ala Thr Pro	Phe 575	Leu Leu Gly Ser	Phe 580	Ile Leu Leu Leu	Val 585
Val Gln Leu His	Trp 590	Glu Gly Gln Leu	Leu 595	Pro Pro Lys Leu	Leu 600
Thr Met Pro Arg	Leu 605	Gly Thr Ser Ala	Thr 610	Thr Asn Pro Pro	Arg 615
His Asn Gly Ala	Tyr 620	Ala Leu Arg Leu	Gly 625	Ile Gly Leu Leu	Leu 630
Cys Thr Arg Leu	Ala 635	Gly Leu Phe His	Arg 640	Cys Pro Glu Glu	Thr 645
Pro Val Cys His	Ser 650	Ser Pro Trp Leu	Ser 655	Pro Leu Ala Ser	Met 660
Val Gly Gly Arg	Ala 665	Lys Asn Leu Trp	Tyr 670	Gly Ala Cys Val	Ala 675
Ala Leu Val Ala	Leu 680	Leu Ala Ala Val	Arg 685	Leu Trp Leu Arg	Arg 690
Tyr Gly Asn Leu	Lys 695	Ser Pro Glu Pro	Pro 700	Met Leu Phe Val	Arg 705
Trp Gly Leu Pro	Leu 710	Met Ala Leu Gly	Thr 715	Ala Ala Tyr Trp	Ala 720
Leu Ala Ser Gly	Ala 725	Asp Glu Ala Pro	Pro 730	Arg Leu Arg Val	Leu 735
Val Ser Gly Ala	Ser 740	Met Val Leu Pro	Arg 745	Ala Val Ala Gly	Leu 750
Ala Ala Ser Gly	Leu 755	Ala Leu Leu Leu	Trp 760	Lys Pro Val Thr	Val 765
Leu Val Lys Ala	Gly 770	Ala Gly Ala Pro	Arg 775	Thr Arg Thr Val	Leu 780
Thr Pro Phe Ser	Gly	Pro Pro Thr Ser	Gln	Ala Asp Leu Asp	Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg Gly	
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
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<213> Homo sapiens

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 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
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 cgtgtgtgat tgggtcatgc atgtaggctt cttacaatg atgggtgggccc 1650  
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcagt 1700  
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10					15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165



<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct

<400> 105  
cgctgctgct gttgctcctg g 21

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 106  
cagtgtgccca ggactttg 18

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 107  
agtcgcaggc agcgttgg 18

<210> 108  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 108  
ctcctccgag tctgtgtgct cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50  
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100  
tctgctgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150  
gctcctgggg ggcccagatc atcggggggc acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttctgtctg cgagcccgtt ggggtgtctc ggccgcccac tgcctcagcc 300  
acagagacct ccgactggc ctggtggtgc tgggcgcca cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccatga cccacgcca cgacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500  
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctgg 550  
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600  
ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650  
cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700  
gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750  
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800  
cccgacgtgt acacgcagggt gtccgccttt gtggcctgga tctgggacgt 850  
ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900  
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
tgttcagggg tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
1				5					10					15

Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30

Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
			35						40					45

Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60

Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65				70						75

Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90

His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105

Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120

Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135

Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150

Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165

Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180

Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195

Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210

Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225

Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240

Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
 275 280

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 112  
 gacgtctgca acagctcctg gaag 24

<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 113  
 cgagaaggaa acgaggccgt gag 23

<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-44  
 <223> Synthetic construct.

<400> 114  
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50  
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200







Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgcctggca tgtggctcctg gggcgcggtt ggcggcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
 agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200  
 cggctgcggg acctgactag attctacgac aaggtaacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaacctctt gcttgcattt actctcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggacctg agggagcagc aagggccctg atgcggctgc 450  
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500  
 agagtactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600  
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700



tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala  
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr  
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg  
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala  
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu  
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe  
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His  
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr  
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly  
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn  
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser  
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr  
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly  
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu  
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser  
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala  
230 235 240



Ser Pro Glu Asp

<210> 119  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 119  
cgggacagga gaccagaaa ggg 23

<210> 120  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 120  
ggccaagtga tccaaggcat cttc 24

<210> 121  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 121  
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122  
<211> 1778  
<212> DNA  
<213> Homo sapiens

<400> 122  
gagataggga gtctgggttt aagtctctgc tccatctcag gagcccctgc 50  
tcccaccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200





	230		235		240
Ile Leu Leu Pro	Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr			
	245	250		255	
Ile Thr Arg Val	Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp			
	260	265		270	
Gly Leu Leu Gly	Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly			
	275	280		285	
Thr Gly Cys Cys	Leu Cys Tyr Pro Asn				
	290				

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcattctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens



<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggcgg gcccggtggac cttcaccctt 100  
ctctgtgggt tgctggcagc caccttgatc caagccaccc tcagtccac 150  
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtctgaagc acatcatctg gctgaaggtc atcacagcta 350  
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggtgga ttcaacacgc ccctggtcaa 450  
gaccatcgtg gaggttccaca tgacgactga ggcccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccacccgcc tggctcctcag tgactgtgcc 550  
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttctt 600  
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700  
ggcatgtatg cagacctcct gcagctgggt aaggtgcccc tttccctcag 750  
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ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850  
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccacctgga 900  
caacatcccg ttcagcctca tctgtagtca ggacgtgggt aaagctgcag 950  
tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000  
cttcttgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050  
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aggacactcc cgagtttttt atagaccaag gccatgcccc ggtggcccaa 1150  
ctgatcgtgc tggaaagtgt tccctccagt gaagccctcc gccctttgtt 1200  
caccctgggc atcgaagcca gctcgaagc tcagttttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
cactgagatc atccactcca tctgtctgcc gaaccagaat ggcaaattaa 1400  
gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500  
 gaaacccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550  
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128  
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala  
     1                    5                    10                    15  
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
                     20                    25                    30  
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
                     35                    40                    45  
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
                     50                    55                    60  
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
                     65                    70                    75  
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
                     80                    85                    90  
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
                     95                    100                    105  
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
                     110                    115                    120  
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
                     125                    130                    135  
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
                     140                    145                    150  
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
                     155                    160                    165  
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
                     170                    175                    180  
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
                     185                    190                    195  
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
                     200                    205                    210  
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
                     215                    220                    225

Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys
				230					235					240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser
				245					250					255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu
				260					265					270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser
				275					280					285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu
				290					295					300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His
				305					310					315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp
				320					325					330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr
				335					340					345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu
				350					355					360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu
				365					370					375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr
				380					385					390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp
				395					400					405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp
				410					415					420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu
				425					430					435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu
				440					445					450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys
				455					460					465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser
				470					475					480
Pro	Val	Ser	Gln											

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129

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gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100  
aaagaaggag atggtgttat ctgaaaagggt tagtcagctg atggaatgga 150  
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
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<210> 130  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens

<400> 130  
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 20 25 30  
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met  
 35 40 45  
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
 50 55 60  
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
 65 70 75  
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
 80 85 90  
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
				320					325					330	
Ser	Phe	Leu	Met	Ser											
				335											

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
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 ctgctaggga gagaacgcca gagggaggcg gctggcccg cggcaggctc 100



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 ataggacaga attattcaaa cggttatagca aatottaggt ggcaccaaga 1650  
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750  
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 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtgggtcac 1850  
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 aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250  
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300  
 atgttccttt aaataataga gaataaaaaa tattgtaata atatgtatca 2350  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450  
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132  
 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala  
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 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
                     20                    25                    30  
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
                     35                    40                    45  
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
                     50                    55                    60  
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
                     65                    70                    75



Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly	80	85	90
Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	95	100	105
Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly	110	115	120
Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	125	130	135
His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	140	145	150
Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	155	160	165
Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	170	175	180
Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	185	190	195
Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	200	205	210
Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	215	220	225
Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	230	235	240
Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	245	250	255
Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn			



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<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

<400> 134  
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 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly





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<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens.

<400> 138  
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 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met  
 20 25 30  
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp  
 35 40 45  
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val  
 50 55 60  
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg  
 65 70 75  
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu  
 80 85 90  
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu  
 95 100 105  
 Cys Arg Ser Val Ser  
 110

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139



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<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
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 20 25 30  
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu





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<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens

<400> 142



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Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro
	305	310	315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg
	320	325	330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser
	335	340	345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala
	350	355	360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu
	365	370	375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His
	380	385	390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala
	395	400	405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro
	410	415	420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala
	425	430	435
Glu Gly His Gly	Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys
	440	445	450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
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 ttttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttccct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
                     20                    25                    30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
                     35                    40                    45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
                     50                    55                    60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
                     65                    70                    75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
                     80                    85                    90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400



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<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60

Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75

Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90

Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105

Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120

Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135

Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150

Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165

Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180

Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195

Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210

Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225

Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240

Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50  
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100  
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttgggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttctctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg 500



ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggt tccccggcc cacagcgaag tggaaaggtc cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgtctatct gagccgagag gtggaatcca gggtagagat 850  
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950  
 ttctttctca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100  
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200  
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaaatcc ccgttttatc agcgtcttcc ccaggacccc acctacaaaa 1400  
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500  
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaaactccc 1550  
 atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttgga 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc cttcctcccc aggggtgaaa ttaggatga atcacatccc 1700  
 acattcttct ttagggatat taaggctctct ctcccagatc caaagtccc 1750  
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800  
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850  
 cattacattt agtttgcctc cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950





<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccggtggc ggtggcggcg gcggttgagg aggccttcctt 50  
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctggggc 150  
gcctcgccct gttgtgctgc gccgcggccg ccgcccgggt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250  
cgcgtgcggc ggccccgggt tgcggggcga gccagccac cccttccta 300  
gggcgacggc tcccacggcc caggccccga ggaccgggccc cccgcgcgcc 350  
accgtccacc gacccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500  
acctctcagg cgcgcgaccag acccgcgccc accacccttt cgacgaccac 550  
tggcccggcg cgcgaccacc ctgtagcgac caccgtaccg gcgcccacga 600  
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650  
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700  
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750  
agaccacagg gcagtgtgag tgcgcggccag gttatcaggg gcttcactgt 800  
gaaacctgca aagagggcct ttacctaaat tacacttctg ggctctgtca 850  
gccatgtgac tgtagtcac atggagctct cagcataccg tgcaacaggt 900  
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaacaa 950  
aaaaggctgc tactctcaag gaccatactg gtttaaacaaggaggatga 1000  
gggtcataga tttaaaaaat attttatata cttttattct cttactttat 1050  
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100  
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150  
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggct 1200  
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250  
atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300  
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350  
ggtaccctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400  
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450  
aactattatg ttatttgag gtaatttaat ctagtggaaat aatgtactgt 1500  
tatctaagca tttgccttgt actgcactga aagtaattat tctttgacct 1550  
tatgtgaggc acttggtttt ttgtggaccc caagtcaaaa aactgaagag 1600  
acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650  
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700  
agtaatttcc tttcactgag cttgtttctt ctcaagggtg ttgtgaagat 1750  
taaagaggt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800  
ctgggttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atactttagc 1900  
 actaaatatt ttaaagtgtt tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050  
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100  
 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250  
 agaggggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153  
 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys  
 1 5 10 15  
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn  
 20 25 30  
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro  
 35 40 45  
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala  
 50 55 60  
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala  
 65 70 75  
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro  
 80 85 90  
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr  
 95 100 105  
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala  
 110 115 120  
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro  
 125 130 135  
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val  
 140 145 150  
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro  
 155 160 165  
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro



<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgagcag ttagacacgtg ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggcttt ggtctcggtg cccagggccc aggcctgtgt gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
 ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200  
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcctgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgcca tcctcttcac tcagctggag 400  
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttctctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600  
 gggctctgtg acctcggcca gtgtccaacc acctcgtca gcggctcccg 650  
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90



Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50  
 gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
 gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttacct 200  
 tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250  
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaattctgac ctgctctgtg ccctgggcct 550  
 gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcattccaca 650  
 gccccaggac catggcacca gcctcacctg tcaggtagacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850  
 tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900  
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950





Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgcc tgtccttcac 100  
 cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagt 200  
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcac 250  
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcca ggaggaccca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550  
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tocagccatg acccttcct 650  
 gctcccacc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
				35					40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
				50					55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
				65					70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
				80					85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
				95					100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
				110					115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
				125					130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
				140					145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
				155					160					165
Cys	Val	Pro	Glu	His										
				170										

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
caggacctg gtacgtgaag gccatggtgg togataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169







<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc ggggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccttga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400



Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181  
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 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-22  
 <223> Synthetic construct.

<400> 181  
 gtgtttctgct ggagccgatg cc 22

<210> 182  
 <211> 18  
 <212> DNA  
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<220>  
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 <222> 1-18  
 <223> Synthetic construct.

<400> 182  
 gacatggaca atgacagg 18

<210> 183  
 <211> 18  
 <212> DNA  
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<220>  
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 <222> 1-18  
 <223> Synthetic construct.

<400> 183  
 cctttcagga tgtaggag 18

<210> 184  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 184  
 gatgtctgcc accccaag 18

<210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 185  
 gcatcctgat atgacttgct acgtggc 27

<210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 186  
 tacaagaggg aagaggagtt gcac 24

<210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-52  
 <223> Synthetic construct.

<400> 187  
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
 cc 52

<210> 188  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens

<400> 188  
 cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50  
 ctcttttgag ctgtgactca gaaaacaaa acttctctgtg ctaagtgcc 100

cccaaagtgt tctgtgtca ataactca ctgcacctgc aacctggat 150  
 atacttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200  
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250  
 aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350  
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 ottgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
 ttcttgtttc atttcgcgac tgccctotca gtgtttcctg ggatcccctc 550  
 ccaaataaag tacttatatt ctc 573

<210> 189  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser  
 1 5 10 15  
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
 20 25 30  
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
 35 40 45  
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
 50 55 60  
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
 65 70

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 190  
 aggaccatt gcttcttcca ggcc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
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gactttggaa gtgaccacc atggggctca gcattctttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtgggctg aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cactctcag 550  
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700  
atgcctgccg ggggtgattct gggggcccc tgggtgtgtg gggagtctt 750  
caaggtcttg tgtcctgggg gtctgtggg ccctgtggac aagatggcat 800





	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
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Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
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 tcgcatgtc gggcgagctc agcaacaggt tocaaggagg gaaggcgctc 150  
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
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 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400  
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 cttccagcct gtgttccct cacttgagg aaccagcact ctccatcctt 900  
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 cctctttcgg gtttccttgg acagtgccat ggttccagt ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
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 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450  
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
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 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn  
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 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu  
 35 40 45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
 50 55 60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
 65 70 75  
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys  
 80 85 90  
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr  
 95 100 105  
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu  
 110 115 120  
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro  
 125 130 135  
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro  
 140 145 150

<210> 197  
 <211> 4842  
 <212> DNA  
 <213> Homo sapiens

<400> 197

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acaacaacat cagtcgcata ctggtcacca gcttcaacca catgccgaag 700  
atccgaactc tgcgcttcca ctccaaccac ctctaactgg actgccacct 750  
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tgtgcgactg ccacttgaag tggctggccg actacctcca ggacaacccc 1450



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 tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300  
 gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcca 4350





	455	460	465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg 470	Ile Ser Gln Ile Lys 475	Ser 480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu 485	Asp Tyr Arg Ser Arg 490	Phe 495
Ser Ser Glu Cys	Phe Met Asp Leu Val 500	Cys Pro Glu Lys Cys 505	Arg 510
Cys Glu Gly Thr	Ile Val Asp Cys Ser 515	Asn Gln Lys Leu Val 520	Arg 525
Ile Pro Ser His	Leu Pro Glu Tyr Val 530	Thr Asp Leu Arg Leu 535	Asn 540
Asp Asn Glu Val	Ser Val Leu Glu Ala 545	Thr Gly Ile Phe Lys 550	Lys 555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu 560	Ser Asn Asn Lys Ile 565	Lys 570
Glu Val Arg Glu	Gly Ala Phe Asp Gly 575	Ala Ala Ser Val Gln 580	Glu 585
Leu Met Leu Thr	Gly Asn Gln Leu Glu 590	Thr Val His Gly Arg 595	Val 600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr 605	Leu Met Leu Arg Ser 610	Asn 615
Leu Ile Ser Cys	Val Ser Asn Asp Thr 620	Phe Ala Gly Leu Ser 625	Ser 630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn 635	Arg Ile Thr Thr Ile 640	Thr 645
Pro Gly Ala Phe	Thr Thr Leu Val Ser 650	Leu Ser Thr Ile Asn 655	Leu 660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys 665	His Leu Ala Trp Leu 670	Gly 675
Lys Trp Leu Arg	Lys Arg Arg Ile Val 680	Ser Gly Asn Pro Arg 685	Cys 690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile 695	Pro Ile Gln Asp Val 700	Ala 705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn 710	Glu Glu Ser Ser Cys 715	Gln 720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys 725	Thr Cys Met Glu Thr 730	Val 735
Val Arg Cys Ser	Asn Lys Gly Leu Arg 740	Ala Leu Pro Arg Gly 745	Met 750



Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys			



Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser  
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

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<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gaggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
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caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
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ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccg ttcctcccaa tttccttct caaacttgga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaat 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
   1                  5                  10                  15  
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
                   20                  25                  30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
                   35                  40                  45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
                   50                  55                  60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
                   65                  70                  75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
                   80                  85                  90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
                   95                  100                 105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
                  110                 115                 120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
                  125                 130                 135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
                  140                 145

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
ctcattggct gcctggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
tcagtgacca aggctgagca ggcg 24

<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcattgtgt aaaaacgcc aactgaatat atcatgcccc 100  
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatatt actgtcaatt cccagatctg cttctcacca 250



<212> PRT  
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	



Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg
				275					280					285
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg
				290					295					300
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr
				305					310					315
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val							
				320										

<210> 211  
 <211> 1554  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
 cttcgcgatc ttccgcgta cttcttctg ggcgttggtg ggagccgtgc 100  
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
 tttgcatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250  
 ccttctggtt tggcaggcgc ctcttggtta gtttgggcac tggtgatgta 300  
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
 agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500  
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600  
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850  
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tgggtacttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200  
 gatcgggttg atgatgaatt agtaatgaaa actttttcct cacttggtt 1250  
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atgggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca ttttaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
 1 5 10 15  
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
 20 25 30  
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
 35 40 45  
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
 50 55 60  
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
 65 70 75  
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
 80 85 90  
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
 95 100 105  
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn  
 110 115 120  
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
 125 130 135  
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

				140					145					150
Asp	Lys	Trp	Leu	Ser 155	Tyr	Pro	Glu	Thr	Gln 160	His	Val	Pro	Leu	Ser 165
Gln	His	Met	Leu	Gly 170	Phe	Ala	Met	Lys	Ser 175	Val	Thr	Gln	Met	Val 180
Met	Gly	Ser	Thr	Phe 185	Glu	Asp	Asp	Gln	Glu 190	Val	Ile	Arg	Phe	Gln 195
Lys	Asn	His	Gly	Thr 200	Val	Trp	Ser	Glu	Ile 205	Gly	Lys	Gly	Phe	Leu 210
Asp	Gly	Ser	Leu	Asp 215	Lys	Asn	Met	Thr	Arg 220	Lys	Lys	Gln	Tyr	Glu 225
Asp	Ala	Leu	Met	Gln 230	Leu	Glu	Ser	Val	Leu 235	Arg	Asn	Ile	Ile	Lys 240
Glu	Arg	Lys	Gly	Arg 245	Asn	Phe	Ser	Gln	His 250	Ile	Phe	Ile	Asp	Ser 255
Leu	Val	Gln	Gly	Asn 260	Leu	Asn	Asp	Gln	Gln 265	Ile	Leu	Glu	Asp	Ser 270
Met	Ile	Phe	Ser	Leu 275	Ala	Ser	Cys	Ile	Ile 280	Thr	Ala	Lys	Leu	Cys 285
Thr	Trp	Ala	Ile	Cys 290	Phe	Leu	Thr	Thr	Ser 295	Glu	Glu	Val	Gln	Lys 300
Lys	Leu	Tyr	Glu	Glu 305	Ile	Asn	Gln	Val	Phe 310	Gly	Asn	Gly	Pro	Val 315
Thr	Pro	Glu	Lys	Ile 320	Glu	Gln	Leu	Arg	Tyr 325	Cys	Gln	His	Val	Leu 330
Cys	Glu	Thr	Val	Arg 335	Thr	Ala	Lys	Leu	Thr 340	Pro	Val	Ser	Ala	Gln 345
Leu	Gln	Asp	Ile	Glu 350	Gly	Lys	Ile	Asp	Arg 355	Phe	Ile	Ile	Pro	Arg 360
Glu	Thr	Leu	Val	Leu 365	Tyr	Ala	Leu	Gly	Val 370	Val	Leu	Gln	Asp	Pro 375
Asn	Thr	Trp	Pro	Ser 380	Pro	His	Lys	Phe	Asp 385	Pro	Asp	Arg	Phe	Asp 390
Asp	Glu	Leu	Val	Met 395	Lys	Thr	Phe	Ser	Ser 400	Leu	Gly	Phe	Ser	Gly 405
Thr	Gln	Glu	Cys	Pro 410	Glu	Leu	Arg	Phe	Ala 415	Tyr	Met	Val	Thr	Thr 420
Val	Leu	Leu	Ser	Val 425	Leu	Val	Lys	Arg	Leu 430	His	Leu	Leu	Ser	Val 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
 455 460

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 ctagatttgt cggcttgcgg ggagacttca ggagtcgctg tctctgaact 50  
 tccagcctca gagaccgccc cccttgtccc cgagggccat gggccgggtc 100  
 tcagggcttg tgccctctcg ctccctgacg ctccctggcg atctggtggt 150  
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcattc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgca ctacgtattg gtacattttt gtctcttgca gtgcccttcc 450  
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600  
 ttccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgtttttag tagtaattaag acttatatac agtttttaggg gacaattaa 750  
 aaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr	
				50					55					60	
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val	
				65					70					75	
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His	
				80					85					90	
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp	
				95					100					105	
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu	
				110					115					120	
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu	
				125					130					135	
Lys	Lys	Lys	Pro	Phe											
				140											

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccggaccc tgccgccctg ccaactatgtc ccgcccgtct atgctgcttg 50  
 cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100  
 gaccggcct gctgcagccc catagtgtccc cggaacgagt ggaaggccct 150  
 ggcatcagag tgcgcccagc acctgagcct gcccttaogc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtgca 300  
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggccctgcgg gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550  
 aactctctc caggcaacca gctctaccac ctcattccaga attggccaca 600  
 ctaccgtcc cctgaggcc ctgctgatcc gcacccatt cctccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	
1				5					10					15	
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	
			20						25					30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	
				35					40					45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	
				50					55					60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	
				65					70					75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	
				80					85					90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	
				95					100					105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	
				110					115					120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	
				125					130					135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	
				140					145					150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	
				155					160					165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	
				170					175					180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	
				185					190					195	

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50  
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100  
tctatctggt catctgtggc caggatgatg gtccctcccg ctcagaggac 150  
cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcggaa 200







Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
 215 220 225  
 Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
 230 235 240  
 Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219  
 <211> 2065  
 <212> DNA  
 <213> Homo sapiens

<400> 219  
 gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50  
 gcaggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100  
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200  
 gcgccgccgc cgccgtcgct cctgcagcgc tgtcgacctt gccgctagca 250  
 tcttcccagag caccgggata ccggggtagg aggcgacgcg ggcgagcacc 300  
 agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350  
 ccgggcgctg tccgcgggtg cggcgctgct gctggctctc acgctgccgg 400  
 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
 aagtgtctgg tgggtgtgca ctogaacccg gccacggact ccaagggctc 500  
 ctcttcctcc ccgctgggga tatcggtccg ggcggccaac tccaaggtcg 550  
 ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650  
 tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
 tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaaga 800  
 tgttactcgt gaagctgccg cgaatggtgt cctgctctac ctagataaag 850  
 aggataaggt ttacctaaaa ctggagaaag gtaatttggt tggaggctgg 900  
 cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950  
 ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000  
 gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
 ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150  
 aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200  
 acttattctg aatttcattt cctgggatta ctgaattagt tacagatgtg 1250  
 gaattttatt tgttttagttt taaaagactg gcaaccaggt ctaaggatta 1300  
 gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgcca 1350  
 agaactgtat actgtgttaa tatattgatt atatttgttt ttattccttt 1400  
 ggaattagtt tgtttgggtc ttgtaaaaaa cttggatttt ttttttcagt 1450  
 aactgggtatt atgttttctc ttaaaataag gtaatgaatg gcttgcccac 1500  
 aaatttacct tgactacgat atcatogaca tgactttctc caaaaaaaaa 1550  
 gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataattt 1600  
 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650  
 aaagttgctt acccaaaaatc taagtgtc atccctgagc ctcagcaaaa 1700  
 cagctcccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750  
 aatgattgat aataaccact ttattaaaaa cctaaggttt ttttttttct 1800  
 cgtagacatg accactttat taactggtgg tgggatgctg ttgtttctaa 1850  
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctggttt 1900  
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950  
 ttcaaataatc ccataatctaa atttagtgca atatcttgtc ttttgtatag 2000  
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050  
 tatatgttaa aaaaa 2065

<210> 220  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 220  
 Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu  
 1 5 10 15  
 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp  
 20 25 30  
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp  
 35 40 45  
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu  
 50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
65 70 75

Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
80 85 90

Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
95 100 105

Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
110 115 120

Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
125 130 135

Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
140 145 150

Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
185 190 195

Phe Leu Val Phe Pro Leu  
200

<210> 221  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 221  
acggctcacc atgggctccg 20

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 222  
aggaagagga gcccttggag tccg 24

<210> 223  
<211> 40

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 223  
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
cgggtggccat gactgcggcc gtgtttcttcg gctgcgcctt cattgccttc 50  
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100  
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150  
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350  
ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400  
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ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500  
gtcattatct tgctgcatgt attctggggc attgtatatt ttgatggctg 550  
tgagaagaaa aagtggggca tcctccttat cgttctctctg acccacctgc 600  
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650  
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gggaggcagc tgccgaagcc tgaaaactctg cctgctctgc caagacaaga 750  
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850  
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900  
ta 902

<210> 225  
<211> 257  
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
1				5					10					15	
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
				245					250					255	

Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226  
cggcaaccag ccgcccac caccgctgcc actgccgcc tgcggggcc 50  
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gagccatctg ggggttctgg ggccaagaa cgtctcgag aaagacgccg 150  
agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200  
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250  
gtctgtgaac gtcctgaaca agcagaaggg ggccgcttg ctgtttgtgg 300  
tccgccagaa ggaggctgtg gtgtccttcc aggtgccct aatcctgca 350  
gggatgtttc agcgcaagta cctctaccaa aaagtggaa gaacctgtg 400  
tcagccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450  
tgtccaccct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500  
atggacgatt ttgtgctcag gactggggag cagttcagct tcaataccac 550  
agcagcacag cccagttact tcaagtatga gttccctgaa ggcgtggact 600  
cggtaattgt caaggtgacc tccaacaagg ccttccctg ctcagtcac 650  
tccattcagg atgtgctgtg tcctgtctat gacctggaca acaacgtagc 700  
cttcacggc atgtaccaga cgatgaccaa gaaggcggcc atcacgtac 750  
agcgcaaaga cttcccagc aacagctttt atgtggtggt ggtggtgaag 800  
accgaagacc aagcctgcgg gggctccctg cctttctacc ccttcgcaga 850  
agatgaaccg gtcgatcaag ggcaccgcca gaaaacctg tcagtgtggt 900  
tgtctcaagc agtcacgtct gaggcatacg tcagtgggat gctcttttgc 950  
ctgggtatat ttctctcctt ttacctgtg accgtcctcc tggcctgctg 1000  
ggagaactgg aggcagaaga agaagacct gctggtggcc attgaccgag 1050  
cctgccaga aagcggtcac cctcgagtcc tggctgattc ttttctggc 1100  
agttccctt atgagggta caactatggc tcctttgaga atgtttctgg 1150  
atctaccgat ggtctggttg acagcgtgg cactggggac ctctcttacg 1200  
gttaccaggg ccgctccttt gaacctgtag gtactcggcc ccgagtggac 1250  
tccatgagct ctgtggagga ggatgactac gacacattga ccgacatcga 1300  
ttccgacaag aatgtcattc gcaccaagca atacctctat gtggctgacc 1350







Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				



Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	620	625	630
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	635	640	645
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	650	655	660
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	665	670	675
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	680	685	690
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	695	700	705
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	710	715	720
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	725	730	735
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	740	745	750
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	755	760	765
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	770	775	780
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	785	790	795
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	800	805	810
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	815	820	825
Arg	Asp	Lys	Ile	Tyr	Val	Phe									830		

<210> 228  
 <211> 2848  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
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 tggagaagga gctctcttct tgcttggcag ctggaccaag ggagccagtc 100  
 ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150  
 gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacctg 250  
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300  
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350  
 ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag 400  
 taccagctac aggtcacccct ggagatgcag gatggacatg tcttgtgggg 450  
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500  
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550  
 ggcatcccct tcctcttctt tgaggcttca gaccgggatg agccaggcac 600  
 agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc 650  
 cttccccaga catgttccag ctggagcctc ggctgggggc tctggccctc 700  
 agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca 750  
 gctgttggtg caggtcaagg acatgggtga ccaggcctca ggccaccagg 800  
 ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta 850  
 gagcctatcc acctggcaga gaatctcaaa gtccataacc cgcaccacat 900  
 ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc 950  
 atccccggg accctttgaa gtgaatgcag agggaaacct ctacgtgacc 1000  
 agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc 1050  
 tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc 1100  
 tggatgatga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc 1150  
 acagtacgca tccctgagct cagtccacca ggtactgaag tgactagact 1200  
 gtcagcagag gatgcagatg cccccggctc cccaattcc cacgttgtgt 1250  
 atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc 1300  
 caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tccactccg 1350  
 agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg 1400  
 cagaggggtg cttcagcagc acgtgtgaag tcgaagtgc agtcacagat 1450  
 atcaatgatc acgcccctga gttcatcact tcccagattg ggcctataag 1500  
 cctccctgag gatgtggagc ccgggactct ggtggccatg ctaacagcca 1550  
 ttgatgctga cctcgagccc gccttcgcc tcattggattt tgccattgag 1600  
 aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg 1650

gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa 1700  
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gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca 1850  
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atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctggct 1950  
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cgggattggc gcctccagac tctcaatggt tcccatgcct acctcacctt 2250  
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gccacaatgc ccagatgtgg cagctcctgg ttcgagtgat cgtgtgtcgc 2350  
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gccacgaag ctgtcggcag tgggcacct tgtaggcacc ctggtagcaa 2450  
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aaggacccg atcaaccagc agacagcgtg cccctgaagg cgactgtctg 2550  
aatggcccag gcagctctag ctgggagctt ggctctggc tccatctgag 2600  
tcccctggga gagagcccag caccgaagat ccagcagggg acaggacaga 2650  
gtagaagccc ctccatctgc cctggggtgg aggcaccatc accatcacca 2700  
ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt 2750  
gctccaaatg tcagggtgtt tgcccaataa taaagcccca gagaactggg 2800  
ctgggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag 2848

<210> 229  
<211> 807  
<212> PRT  
<213> Homo sapiens

<400> 229  
Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln  
1 5 10 15  
Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

	20	25	30
Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro	35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp	50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser	65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala	80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val	95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn	110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu	125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala	140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe	155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe	170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly	185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu	200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala	215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser	230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro	245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr	260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu	275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala	290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp	305	310	315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440					445					450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485					490					495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500					505					510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515					520					525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
				575					580					585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	





<220>  
<221> Artificial Sequence  
<222> full  
<223> Synthetic oligonucleotide probe

<400> 231  
cctgagctgt aaccccactc cagg 24

<210> 232  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 232  
agagtctgtc ccagctatct tgt 23

<210> 233  
<211> 2786  
<212> DNA  
<213> Homo sapiens

<400> 233  
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atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100  
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
acttgaagct caatttcttg aaatctccct cctccttcaa tcggcctgtg 200  
gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttcctgag 250  
atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300  
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350  
agtaataact tcaactacgg ggcttaccat tccctggaag ctattttacca 400  
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450  
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550  
ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600  
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700  
tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750  
gctcctgcat tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800  
ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850









aatcaccaaa ccatcaacag ggaccccagt cacaagccaa cacccattaa 1500  
 cccagtcag tgcccttttc cacaatttct cccaggtaac tagcttcatg 1550  
 ggatgttgct gggttaccat atttcattc cttggggctc ccaggaatgg 1600  
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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys  
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 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
                   20                  25                  30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
                   35                  40                  45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
                   50                  55                  60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
                   65                  70                  75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
                   80                  85                  90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
                   95                  100                  105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
                   110                  115                  120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
                   125                  130                  135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
                   140                  145                  150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
                   155                  160                  165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
                   170                  175                  180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
                   185                  190                  195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

	200		205		210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe		
	215	220	225		
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met		
	230	235	240		
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn		
	245	250	255		
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe		
	260	265	270		
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala		
	275	280	285		
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys		
	290	295	300		
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser		
	305	310	315		
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala		
	320	325	330		
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser		
	335	340	345		
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser		
	350	355	360		
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile		
	365	370	375		
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn		
	380	385	390		
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile		
	395	400	405		
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser			
	410	415			

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 238  
ctttgctggtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 239  
tgactcgggg tctccaaaac cagc 24

<210> 240  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 240  
ggtataggcg gaaggcaaag tcgg 24

<210> 241  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 241  
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242  
<211> 2436  
<212> DNA  
<213> Homo sapiens

<400> 242  
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50











gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

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tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
ccccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200  
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350  
tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400  
gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450  
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tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800  
acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
gttgtcacat cagctgacat gacctggagg gggtgggggt gggggacagg 900  
tttctgaaat ccctgaaggg gggtgtactg ggatttgtga ataaacttga 950  
tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
230 235 240

Ser Val Ala Asn Ile Met Pro  
245

<210> 249  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 249  
caatatgcat cttgcacgtc tgg 23

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 250  
aagcttctct gcttcctttc ctgc 24

<210> 251  
<211> 43  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-43  
<223> Synthetic construct.

<400> 251  
tgacccatt gagaaggtca ttgaaggat caaccgagg ctg 43

<210> 252  
<211> 3781  
<212> DNA  
<213> Homo sapiens

<400> 252

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tgaccctgac tcaactccagg tccggaggcg ggggcccccg gggcgactcg 150  
ggggcggaacc gcggggcgga gctgcgcgcc gtgagtcagg ccgagccacc 200  
tgagcccgag ccgcgggaca ccgtcgtctc tgctctccga atgctgcgca 250  
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<210> 253  
 <211> 837  
 <212> PRT  
 <213> Homo sapiens

<400> 253  
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu  
 20 25 30  
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser  
 35 40 45  
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
 50 55 60  
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu  
 65 70 75  
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu



Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380		385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395		400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
410		415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
425		430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
440		445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
455		460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
470		475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
485		490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
500		505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
515		520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
530		535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
545		550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
560		565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
575		580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
590		595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
605		610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
620		625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
635		640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
650		655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val



<400> 255  
tgaagccagg gcagcgtcct ctgg 24

<210> 256  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 256  
gtacaggctg cagttggc 18

<210> 257  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 257  
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 258  
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259  
<211> 4563  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 3635  
<223> unknown base

<400> 259  
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agggcgggac gggagcccgg actcgtctgc cgccgccgtc gtcgccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200  
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 caggccgcgg cggcgggggc ggggtgtcgg aacaaagcgc cgccgcgggg 300  
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 attttttgta tgatcagttt ttgaagtccg tatacaagga tatattttac 3000  
 aagtggtttt cttacatagg actcctttta gattgagctt tctgaacaag 3050



aaggatgatca gtgtttgcct ttgaacacat cttcttgctg aacattatgt 3100  
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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro  
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly  
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser  
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly  
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala  
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe  
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro  
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe  
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu  
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg  
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe  
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu  
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val  
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly  
230 235 240

Lys	Cys	Leu	Arg	Glu 245	Met	Tyr	Thr	Thr	His 250	Glu	Asp	Val	Glu	Val 255
Gly	Arg	Cys	Val	Arg 260	Arg	Phe	Ala	Gly	Val 265	Gln	Cys	Val	Trp	Ser 270
Tyr	Glu	Met	Arg	Gln 275	Leu	Phe	Tyr	Glu	Asn 280	Tyr	Glu	Gln	Asn	Lys 285
Lys	Gly	Tyr	Ile	Arg 290	Asp	Leu	His	Asn	Ser 295	Lys	Ile	His	Gln	Ala 300
Ile	Thr	Leu	His	Pro 305	Asn	Lys	Asn	Pro	Pro 310	Tyr	Gln	Tyr	Arg	Leu 315
His	Ser	Tyr	Met	Leu 320	Ser	Arg	Lys	Ile	Ser 325	Glu	Leu	Arg	His	Arg 330
Thr	Ile	Gln	Leu	His 335	Arg	Glu	Ile	Val	Leu 340	Met	Ser	Lys	Tyr	Ser 345
Asn	Thr	Glu	Ile	His 350	Lys	Glu	Asp	Leu	Gln 355	Leu	Gly	Ile	Pro	Pro 360
Ser	Phe	Met	Arg	Phe 365	Gln	Pro	Arg	Gln	Arg 370	Glu	Glu	Ile	Leu	Glu 375
Trp	Glu	Phe	Leu	Thr 380	Gly	Lys	Tyr	Leu	Tyr 385	Ser	Ala	Val	Asp	Gly 390
Gln	Pro	Pro	Arg	Arg 395	Gly	Met	Asp	Ser	Ala 400	Gln	Arg	Glu	Ala	Leu 405
Asp	Asp	Ile	Val	Met 410	Gln	Val	Met	Glu	Met 415	Ile	Asn	Ala	Asn	Ala 420
Lys	Thr	Arg	Gly	Arg 425	Ile	Ile	Asp	Phe	Lys 430	Glu	Ile	Gln	Tyr	Gly 435
Tyr	Arg	Arg	Val	Asn 440	Pro	Met	Tyr	Gly	Ala 445	Glu	Tyr	Ile	Leu	Asp 450
Leu	Leu	Leu	Leu	Tyr 455	Lys	Lys	His	Lys	Gly 460	Lys	Lys	Met	Thr	Val 465
Pro	Val	Arg	Arg	His 470	Ala	Tyr	Leu	Gln	Gln 475	Thr	Phe	Ser	Lys	Ile 480
Gln	Phe	Val	Glu	His 485	Glu	Glu	Leu	Asp	Ala 490	Gln	Glu	Leu	Ala	Lys 495
Arg	Ile	Asn	Gln	Glu 500	Ser	Gly	Ser	Leu	Ser 505	Phe	Leu	Ser	Asn	Ser 510
Leu	Lys	Lys	Leu	Val 515	Pro	Phe	Gln	Leu	Pro 520	Gly	Ser	Lys	Ser	Glu 525
His	Lys	Glu	Pro	Lys	Asp	Lys	Lys	Ile	Asn	Ile	Leu	Ile	Pro	Leu

				530					535					540
Ser	Gly	Arg	Phe	Asp 545	Met	Phe	Val	Arg	Phe 550	Met	Gly	Asn	Phe	Glu 555
Lys	Thr	Cys	Leu	Ile 560	Pro	Asn	Gln	Asn	Val 565	Lys	Leu	Val	Val	Leu 570
Leu	Phe	Asn	Ser	Asp 575	Ser	Asn	Pro	Asp	Lys 580	Ala	Lys	Gln	Val	Glu 585
Leu	Met	Arg	Asp	Tyr 590	Arg	Ile	Lys	Tyr	Pro 595	Lys	Ala	Asp	Met	Gln 600
Ile	Leu	Pro	Val	Ser 605	Gly	Glu	Phe	Ser	Arg 610	Ala	Leu	Ala	Leu	Glu 615
Val	Gly	Ser	Ser	Gln 620	Phe	Asn	Asn	Glu	Ser 625	Leu	Leu	Phe	Phe	Cys 630
Asp	Val	Asp	Leu	Val 635	Phe	Thr	Thr	Glu	Phe 640	Leu	Gln	Arg	Cys	Arg 645
Ala	Asn	Thr	Val	Leu 650	Gly	Gln	Gln	Ile	Tyr 655	Phe	Pro	Ile	Ile	Phe 660
Ser	Gln	Tyr	Asp	Pro 665	Lys	Ile	Val	Tyr	Ser 670	Gly	Lys	Val	Pro	Ser 675
Asp	Asn	His	Phe	Ala 680	Phe	Thr	Gln	Lys	Thr 685	Gly	Phe	Trp	Arg	Asn 690
Tyr	Gly	Phe	Gly	Ile 695	Thr	Cys	Ile	Tyr	Lys 700	Gly	Asp	Leu	Val	Arg 705
Val	Gly	Gly	Phe	Asp 710	Val	Ser	Ile	Gln	Gly 715	Trp	Gly	Leu	Glu	Asp 720
Val	Asp	Leu	Phe	Asn 725	Lys	Val	Val	Gln	Ala 730	Gly	Leu	Lys	Thr	Phe 735
Arg	Ser	Gln	Glu	Val 740	Gly	Val	Val	His	Val 745	His	His	Pro	Val	Phe 750
Cys	Asp	Pro	Asn	Leu 755	Asp	Pro	Lys	Gln	Tyr 760	Lys	Met	Cys	Leu	Gly 765
Ser	Lys	Ala	Ser	Thr 770	Tyr	Gly	Ser	Thr	Gln 775	Gln	Leu	Ala	Glu	Met 780
Trp	Leu	Glu	Lys	Asn 785	Asp	Pro	Ser	Tyr	Ser 790	Lys	Ser	Ser	Asn	Asn 795
Asn	Gly	Ser	Val	Arg 800	Thr	Ala								

<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 261  
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<210> 262  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
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gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccctattc 500  
 tggctgatca aaccaaaca tgtttccatt gttttgcatg cagaggaacc 550  
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaac 600  
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650  
 ccatatgtta cctcatataa gtcacctgtc accacttttag ataagagcac 700  
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcagggtg 750  
 aaactgcatg agaaaaaccc gaagagtttg gaaagcacc agagagttgg 800  
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgc 850  
 acaggcactt cttagtaca ccagcaaccc agcatataga gaagatattg 900  
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
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 aaaaatttta aacctacttg atattccata acaaagctga ttttaagcaaa 1250  
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 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
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 attttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1				5					10					15

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



Leu Leu Lys Val Tyr  
350

<210> 266  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 266  
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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcactg 200  
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250  
tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300  
caggaatcag ttccatgtct tgggtccact ctacagagat ggggaagact 350  
gggaatctaa gcagatgcc aagtatcgag ggagaactga gtttgtgaag 400  
gactccattg caggggggag tgtctctcta aggctaaaaa acatcactcc 450  
ctcggacatc ggctgtatg ggtgtgtgtt cagttcccag atttacgatg 500  
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aggatttgtc ttcagactcc agagcaaagt cagatgggta cagcctgtat 700  
gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750  
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taggagagac gtttttccag ccctcacctt ggcgctggc ttctatttta 850  
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gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000  
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gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100  
agagatttac aaggaagagt gtggtggctt ctcaagggtt ccaagcaggg 1150  
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200  
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250





	20	25	30
Leu Val Gly Glu Asp	Ala Val Phe Ser Cys	Ser Leu Phe Pro Glu	
35	40	45	
Thr Ser Ala Glu Ala	Met Glu Val Arg Phe	Phe Arg Asn Gln Phe	
50	55	60	
His Ala Val Val His	Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser	
65	70	75	
Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp	
80	85	90	
Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr	
95	100	105	
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile	
110	115	120	
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly	
125	130	135	
Ser Leu Pro Leu Ile	Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile	
140	145	150	
Gln Leu Leu Cys Leu	Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala	
155	160	165	
Lys Trp Lys Gly Pro	Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg	
170	175	180	
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile	
185	190	195	
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His Leu	
200	205	210	
Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly Glu	
215	220	225	
Thr Phe Phe Gln Pro	Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu	
230	235	240	
Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met Ile	
245	250	255	
Ile Val Phe Phe Lys	Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp	
260	265	270	
Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys	
275	280	285	
His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro Lys	
290	295	300	
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala Pro	
305	310	315	

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 gtcacattca tatccctgat tgcctggca gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350  
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450  
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500



atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatattat 2050  
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 cca 2103

<210> 269  
 <211> 423  
 <212> PRT  
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 20 25 30  
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
 35 40 45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
 50 55 60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
 65 70 75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
 80 85 90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
 95 100 105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
 110 115 120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
 125 130 135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
 140 145 150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
 155 160 165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
 170 175 180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
 185 190 195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
 200 205 210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
 215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415					420
Thr Gly Ile														

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

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<210> 271  
<211> 238  
<212> PRT  
<213> Homo sapiens

<400> 271  
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Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala  
35 40 45  
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys  
50 55 60  
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly  
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
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Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
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Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
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Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
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Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
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Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
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 <212> DNA  
 <213> Homo sapiens

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 tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500



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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser



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Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
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Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
				305					310					315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
				320					325					330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335					340					345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350					355					360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365					370					375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380					385					390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
				395					400					405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
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 <212> DNA  
 <213> Homo sapiens

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<210> 277  
<211> 761  
<212> PRT  
<213> Homo sapiens  
<400> 277



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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				



Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
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Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
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Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 278  
 ctgctggtga aatctggcgt ggag 24

<210> 279  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 279  
 gtctggtcct ggctgtccac ccag 24  
  
 <210> 280  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 280  
 catcttgtca tgtacctggg aaccaccaca gggtogetcc acaag 45  
  
 <210> 281  
 <211> 2320  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
 aggggtccctt agccgggagc agggcgcgca gccagggctg agatccgcgg 50  
 cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100  
 ttctttctcc ctggggctct gctctcagag gctgccaaaa tcttgacaat 150  
 atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
 ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250  
 ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300  
 ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
 tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
 aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450  
 ggatatcatg gattccttaa agaattgagaa ctgcgacatg gtgatagttg 500  
 aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550  
 tttgtggcca ttctttccac ttcatcggc tctttggaat ttgggctacc 600  
 aatccccttg tcttatgttc cagtattccg ttcttctgtg actgatcaca 650  
 tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700  
 aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
 tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800  
 agttgtgggt cattaaactct gactttgcct ttgattttgc tcgacctctg 850  
 cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900



<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly



<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
tgcctttgct cacctacccc aagg 24

<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggt ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50  
ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100  
cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150  
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200  
cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
tgctgtcact gcatgctctg ccaaggagga gggaaactgca gtgacagcag 300  
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400  
ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450



gggttgcaga gccctcagc catgttggga gccaaagccac actggctacc 500  
 aggtccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550  
 tgggggccgg gtggggccag gaggggtcag agcccgctct gctggagggg 600  
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 gggagcagcc ctgggagagg cccccctgg gcgagtggca tttgctgcgg 700  
 tccgaagcca ccacatgag ccagcagggg aaaccggcaa tggcaccagt 750  
 ggggccatct acttcgacca ggtcctggtg aacgagggcg gtggctttga 800  
 ccgggcctct ggctccttcg tagccccgtt ccgggggtgtc tacagcttcc 850  
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000  
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
 tactcaagtt tctctggctt cctcatcttc cctctctgag gaccgaagtc 1100  
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150  
 cccagaaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200  
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300  
 ccctcccagc cacctgtgtc atctgttctt gcctgcagcc ctaggatcag 1350  
 ggcaagggtt ggcaagaagg aagatctgca ctactttggg gcctctgctc 1400  
 ctccggttcc cccacccag cttcctgctc aatgctgac agggacaggt 1450  
 ggcgcaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600  
 aggctcagcc acaggcagaa gggtggaag ggctggagt ctgtggctgg 1650  
 tgaggaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700  
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtcttctat 1750  
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800  
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatgaaa acatcgataa ccatgcatcc tottgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000  
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050  
 gctgtcttat tctcctcctt aggccttcta ttacctggga ttccatgatt 2100  
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200  
 caactagaga atggtgggtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170	175	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser			
	185	190	195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu			
	200	205	

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgtact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50  
 tagccgccca gcctcgacgc cgtcccggga ccctgtgct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150



<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile	Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val Leu Glu Val Asn	
380	385	

<210> 293  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 293  
 gctgacctgg ttcccatcta ctcc 24

<210> 294  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 294  
 cccacagaca cccatgacac ttcc 24

<210> 295  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

<400> 296  
gggcggcgagg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50  
ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100  
cggggcccgcg gaggcgacgc cggggacgcc cgcgcgacga gcagggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggcctg 250  
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300  
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350  
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400  
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
actggctcatg ctgctggagt ggtggctcctg cacggagtgt acactgttca 500  
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
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gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650  
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ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100  
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

tttccagggg agcagtttaa gcctgcccgg aggccgtgga ccctcctgaa 1200  
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 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750  
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800  
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850  
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 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950  
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000  
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050  
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100  
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150  
 ggggtcaggc tgatctcaa ctcctgagtt caggatgatc gcccgacctca 2200  
 gcctccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250  
 atttcttttt aaggctgaat gatgggggac aggcacgatg gctcacgcct 2300  
 gtgatcccaa gtagcttgga ttgtaaacat gcaccaccat gcctggctaa 2350  
 tttttgtatt ttagtagag acgtgttagc caggctggtc tcgatctcct 2400  
 gacotcaagt gaccacctgc ctcagcctcc caaagtactg ggattacagg 2450  
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500  
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550  
 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600





Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 298  
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<210> 299  
 <211> 21  
 <212> DNA





<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100  
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200  
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350  
 ctctcgctgg agcagtgcc tcaccaactg tctcagctct ggaggcactg 400  
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450  
 tgggccttgc cctggccgta gaagggattg acaagccga agatttcata 500  
 ggcgatggct cccactgccc aggcacagc cttgctgtag tcaatcactg 550  
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 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650  
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tgctccagc aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
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 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
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<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
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 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro  
 65 70 75  
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala  
 80 85 90  
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly  
 95 100 105  
 Arg Arg Arg Asp

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305

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 ccgccttcgc cactggcctc ttcttgggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
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 ggctgctgac cctggagcag ccgcaggggg attctatgat gacctgcgag 350  
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 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala  
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 Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe  
 20 25 30  
 Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys  
 35 40 45  
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser  
 50 55 60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
Leu	Thr	Leu	Ala	Phe	Lys	Ile									260		

<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150
ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctggggaccca aggacctgtt cccctacgac 250

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gctggccggg gaggaggccc ccaggagaa ggcggaggac aagcccagca 1850  
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900  
agcgcagagg acaaggagca cgaggaggt cgggactcgg aggagggggc 1950  
aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000  
acctggacag gcctgggagc gaccggcagg agcgcgagag ggcacggggg 2050  
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gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccott 2200  
gggttttttt ttctgccta atttctgtga tttccaacca acatgaaatg 2250  
actataaacg gttttttaat ga 2272

<210> 308  
<211> 671  
<212> PRT  
<213> Homo sapiens

<400> 308  
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Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Asp Ile Ala Asp  
20 25 30  
Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe  
35 40 45  
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro  
50 55 60  
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys  
65 70 75  
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala  
80 85 90  
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala  
95 100 105  
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp  
110 115 120  
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala  
125 130 135  
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser



Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr  
 440 445 450  
 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys  
 455 460 465  
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser  
 470 475 480  
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg  
 485 490 495  
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser  
 500 505 510  
 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys  
 515 520 525  
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala  
 530 535 540  
 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile  
 545 550 555  
 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys  
 560 565 570  
 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala  
 575 580 585  
 Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala  
 590 595 600  
 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu  
 605 610 615  
 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg  
 620 625 630  
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro  
 635 640 645  
 Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala  
 650 655 660  
 Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser  
 665 670

<210> 309  
 <211> 3871  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
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 cagcctcaat aattatatta aattaacacc atttgaaaga gaacattggt 100





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 cacagagaga agttggtgct tagttatgtg ttttttagag tatatactaa 3150  
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 aaattctggc ttgggggaaa actcatatcc ccatgaaaag gaagaacaat 3350  
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<210> 310  
 <211> 777  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
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 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu  
 35 40 45  
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro  
 50 55 60  
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu  
 65 70 75  
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile





Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile	380	385	390
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro	395	400	405
Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

	665		670		675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu				
680	685			690	
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu				
695	700			705	
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu				
710	715			720	
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp				
725	730			735	
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp				
740	745			750	
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His				
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Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr				
770	775				

<210> 311  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 311  
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<210> 312  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 312  
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<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 313  
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<210> 314  
<211> 3934  
<212> DNA  
<213> Homo sapiens

<400> 314  
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accagcacgg cgaggtaggc tttgtccctg agcgatatct caacttccc 1250



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<210> 315  
 <211> 370  
 <212> PRT  
 <213> Homo sapiens

<400> 315  
 Met Gln Leu Ala Lys Tyr Gln Ser His Ser Lys Ser Cys Pro Thr  
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

	305		310		315
Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro	Gly		
	320	325	330		
Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met Ala	Pro		
	335	340	345		
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys	Ala		
	350	355	360		
Pro Asp Pro Gly	His Pro Asp Pro Leu	Thr			
	365	370			

<210> 316  
 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

<400> 316  
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 aagcggccca gacagagtcc tacagaggga gaggccagag aagctgcaga 150  
 agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200  
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catgttggcc aggtgtgtct cgaactcctg accttaggtg atccactcgc 3950  
cttcatctcc caaagtgtct ggattacagg cgtgagccac cgtgcctggc 4000  
cacgccaac taatTTTTgt atttttagta gagacagggt ttcacatgt 4050  
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ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300  
aataaagaac tagcataaca ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400  
aaggaaa 4407

<210> 317  
<211> 837  
<212> PRT  
<213> Homo sapiens

<400> 317  
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg  
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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro  
20 25 30  
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu  
35 40 45  
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu  
50 55 60  
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75  
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90  
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105  
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120  
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135  
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu



Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp					
	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr					
	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro					
	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg					
	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro					
	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					
	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys					
	830		835		

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cggcgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

<400> 321  
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgtttggta tcttgccct aactctaatt gtctgtttt 200  
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
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gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
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gaccatgtat tggatcaatc ccaacttaat atcagtttct gagttacaag 650  
actttgagga ggaggagaa gatcttact ttctgcaa cgaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtggc cctcaagtga aagtagagaa 750  
gaccgcgtac gccagacaag caagtgagga agaacttcca ataatgact 800  
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<210> 322

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Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val  
35 40 45

Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys  
50 55 60

Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys  
65 70 75

Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe  
80 85 90

Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe  
95 100 105

Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys  
110 115 120

Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro  
125 130 135

Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe  
140 145 150

Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn  
155 160 165

Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn  
170 175 180

Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu  
185 190 195

Leu Gln Asp Phe Glu Glu Gly Glu Asp Leu His Phe Pro Ala  
200 205 210

Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro  
215 220 225

Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu  
230 235 240

Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe  
245 250 255

Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg  
260 265 270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaatgt 950  
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Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
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 gtctctgggtg ccattggcct cctgggtatcc atctttgccc tgaaatgcat 400  
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 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500  
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 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328  
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 20 25 30  
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 35 40 45  
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile  
 50 55 60  
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met  
 80 85 90  
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu  
 110 115 120  
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile  
 125 130 135  
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn  
 140 145 150  
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu  
 155 160 165  
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
 170 175 180  
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr  
 185 190 195  
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His  
 200 205 210



gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu  
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp  
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val  
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly  
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln  
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val  
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr  
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr  
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro  
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro  
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr  
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu  
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His  
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly  
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val  
215 220

<210> 331

<211> 1160

<212> DNA



<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50  
ttotacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100  
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttg 150  
gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtgg 200  
ggagtatcag cttttgttg cagcaacatt attgtctttg agaggctctg 250  
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300  
gcaagttcta tagctccttg ttggctctcc cgctgccct ggaaacagcc 350  
cgggccctca tgtgtgtggc tgttgcctc tccttgatcg ccctgcttat 400  
tggcatctgt ggcataagc aggtccagt caccaggctc aacgagagg 450  
ccaaagcata cttctgga acttcaggag toctcttcat cctgacgggt 500  
atcttcgttc tgattccggt gagctggaca gccaatataa tcatacagaga 550  
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600  
cacttttct tggctggga agcgtgctg toctcttcat tggaggggg 650  
ctgctttgtg gattttgctg ctgcaacaga aagaagcaag ggtacagata 700  
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750  
caatgcttag taagacctc accagttatg tctaatacct ctttttggt 800  
ccaagtatgg actatggtca atgtttttta taaagtctg ctagaaactg 850  
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900  
cgaaagtttc aatttggtac tgggtgtagg aatgaaaatg acttacttg 950  
acattctgac ttcaggtgta ttaaatacat tgactattgt tggaccaat 1000  
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100  
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150  
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50  
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100  
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200  
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250  
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300  
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350  
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400  
 ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgcgcga tggtgcctc cccgcgcgg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tctgtgtgtg gggcccaggt 150

ggcataagt gaaataaaact caagctgatg ottcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcatgtatc tcctaatagcc ttacactact tggtttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
 gaagagttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700  
 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 336  
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
 1 5 10 15  
 Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser  
 20 25 30  
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
 35 40 45  
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
 50 55 60  
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
 65 70 75  
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
 80 85 90  
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
 95 100 105  
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
 110 115 120  
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
 125 130 135  
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
 140 145

<210> 337  
 <211> 1310  
 <212> DNA  
 <213> Homo sapiens

<400> 337  
 cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50  
 agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100  
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg ottgcctgcc 150  
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200  
 gaccactgc ccagccgctc agggaccca acgcatccc agcccagcgc 250



Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp  
 50 55 60  
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg  
 65 70 75  
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr  
 80 85 90  
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu  
 95 100 105  
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp  
 110 115 120  
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly  
 125 130 135  
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly  
 140 145 150  
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys  
 155 160 165  
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro  
 170 175 180  
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile  
 185 190 195  
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu  
 200 205 210  
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala  
 215 220 225  
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala  
 230 235 240  
 Phe Ala Met Tyr Arg Pro  
 245

<210> 339  
 <211> 849  
 <212> DNA  
 <213> Homo sapiens

<400> 339  
 gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50  
 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100  
 caagacccta agaaccatca gccctcagct gcacctctc ccctccaagg 150  
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200  
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350  
tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500  
gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550  
caggccggcc actctctac tggctgacag gatgccgcct gagatgaaac 600  
agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650  
ggattottca tttottcttc ctactgcctc cacttcatgt tattttcttc 700  
ccttcccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750  
tcttggtctc ctcttactc ccatctggac ccagtcccct ggttcctgtc 800  
tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 340  
Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala  
1 5 10 15  
Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val  
20 25 30  
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
35 40 45  
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
50 55 60  
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
65 70 75  
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
80 85 90  
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
95 100 105  
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
110 115 120  
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
125 130 135  
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.

<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 343  
atctcaggcg gcacccctgtc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24

<210> 345  
<211> 45  
<212> DNA  
<213> Artificial



<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gcctgcttg 50  
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta ttttttccc 150  
aaggagaaaa ccggggtaaa gggagggaag caattcaatt tgaagtccct 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
ttgcacacgc tgttgcaaa tgtcaggacc aggttaagtg actggcagaa 350  
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400  
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450  
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500  
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatgg 550  
ggcgtgttg caccctcccc accacaccct gcaccagact gtcacagccc 600  
aagccagcaa gcacagccct gaagccagg accgcctgga ctttggggaa 650  
tcccaggatt gggactgga agctgaggat gaggggtgaag agtacagccc 700  
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750  
tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800  
ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850  
cccaaagagg gactgggggg ctgatgagga cggggagggtg tctgaagaag 900  
aggagttgac ccggttcagc ctggaccac gtggcctcca ggaggcactc 950  
agtgcctgca tccccctcca gagggctctg cccgagggtgc ggcaccact 1000  
gtgtctgcag cagcacctc aggacagcct gccacagcc agcgtcatcc 1050  
tctgtttcca tgatgaggcc tggctcactc tctgcggac tgtacacagc 1100



tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15

Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30

Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45

Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60

Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75

Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90

Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105

Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120

Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135

Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150

Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165

Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180

Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195

Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210

Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225

Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240

Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
 tatgtcgtcg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351  
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50  
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100  
tcctctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150  
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200  
caggggagggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250  
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300  
cctggcactg cccccccagc cccccatca ggctttgagg aggggccgcc 350  
ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400  
aggatggagg ggacccaac tctgccaatc ccgatttct ggactatggt 450  
tttgagccc ctcatgggct cgcaaccca caccctaact cagactccat 500  
gcgaggatgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550  
ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600  
gtcacaatta ccatctccat catcattgtt ctctgtggcca ctggcatcat 650  
cttcaagttc tgctgggacc gcagccagaa ggcagcgaga ccctcagggc 700  
agcaagggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750  
tccccggctg gagtcaactgt gctggggggc ttcggggact cacctacccc 800  
caccctgac catgaggagc ccgagggggg acccggcct gggatgcccc 850  
acccaaggg ggctccagcc ttccagttga accggtgagg gcaggggcaa 900  
tgggatggga gggcaaagag ggaaggcaac ttaggtcttc agagctgggg 950  
tgggggtgcc ctctggatgg gtagtgagga ggcaggcgtg gcctcccaca 1000  
gcccctggcc ctccaaggg ggctggacca gctcctctct gggaggcacc 1050  
cttcttctc ccagtctctc aggatctgtg tcctattctc tgctgcccac 1100  
aactccaact ctgccctctt tggtttttct tcatgccacc ttgtctaaga 1150  
caactctgcc ctcttaacct tgattcccc tctttgtctt gaacttcccc 1200  
ttctattctg gcctaccctt tggttcctga ctgtgccctt tcctcttcc 1250  
tctcaggatt cccctggtga atctgtgatg cccccaatgt tggggtgcag 1300

ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350  
 ggcagctgtg gggagctggg gccacagggg ctccctggctc ctgccccttg 1400  
 cacaccaccc ggaacactcc ccagccccac gggcaatcct atctgctcgc 1450  
 cctcctgcag gtgggggcct cacatatctg tgacttcggg tccctgtccc 1500  
 cacccttggtg cactcacatg aaagccttgc aactcacct ccaccttcac 1550  
 aggccatttg cacacgctcc tgcaccctct ccccgctccat accgctccgc 1600  
 tcagctgact ctcatgttct ctggtctcac atttgcactc tctccttccc 1650  
 acattctgtg ctacgctcac tcagtgggtca gcgtttcctg cacactttac 1700  
 ctctcatgtg cgtttcccg gctgatgttg tgggtggtgtg cggcgtgctc 1750  
 actctctccc tcatgaacac ccaccacct cgtttccgca gccctgcgt 1800  
 gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggccctca 1850  
 tcggtcatgg tctgtccca ttccacacca tttgtttctc tgtctccca 1900  
 tcctactoca aggatgcgg catcacctg agggctcccc cttgggaatg 1950  
 gggtagtgag gccccagact tcacccccag cccactgcta aaatctgttt 2000  
 tctgacagat gggttttggg gagtgcctg ctgcactaca tgagaaagg 2050  
 actcccattt gcccttcct ttctctaca gtcccttttg tcttgtctgt 2100  
 cctggctgtc tgttgtgtg ccattctctg gacttcagag cccctgagc 2150  
 cagtcctccc ttcccagcct cctttgggc ctccctaact ccacctaggc 2200  
 tgccaggac cggagtcagc tggttcaagg ccacgggag ctctgcctcc 2250  
 aagtctaccc ttcccttccc ggactccctc ctgtccctc ctttctctcc 2300  
 tccttcctc cactctcct ccttttgctt cctgcccct tccccctcct 2350  
 caggttcttc cctccttctc actggtttt ccaccttct ccttcccttc 2400  
 ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450  
 ttcttggtgat gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500  
 tcaaataaag cctttgcaag ataa 2524

<210> 352  
 <211> 243  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
 1 5 10 15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
				20					25					30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 353  
 <211> 480  
 <212> DNA  
 <213> Homo sapiens

<400> 353  
 gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg cctcactcc 50  
 cggccaggat ggcacctgt ctggccctgc gcatggcgct gctgctggtc 100



tccgggggttc tggccccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgtga 350  
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
     1                    5                    10                    15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
                     20                    25                    30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
                     35                    40                    45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
                     50                    55                    60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
                     65                    70                    75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
                     80                    85                    90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
                     95                    100                    105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
                     110                    115                    120

Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
 ggccgttggt tggcgcgagg ctgaaggggtg tggcgcgagc agcgtcgttg 50  
 gttggccggc ggcgggcccgg gacggggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcaactg cacagcaact 150  
tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200  
tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250  
cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300  
agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350  
taccagggga agatgtactt ccccggtat ttcccaacg agctgcgaaa 400  
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450  
acctggcacc aggcagctgg ggaggaggcg agctctccag ggagggaccc 500  
agcctagcac ctgaaggatc aatgccatca ccccgogggg acctccccta 550  
agtagccccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600  
tgctccatct cacgctgggg gtcaacctgg ggaccccttc cctccgggccc 650  
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700  
tggcatcttc cagtacgaga ccctctctg caacaactgc acagactcgc 750  
acgtcgcttg ctttggctat aactgcgagt agggctcagg catcacaccc 800  
acctgtgcca gggccctact gtccctgggg tcccaggctc tccttgaggg 850  
gggctccccg ccttcacct ggctgtcatc gggtagggcg gggccgtggg 900  
ttcaggggcg caccattcc aagcctgtgt cccacaggtc ctcgggcgag 950  
tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcacia 1000  
gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050  
cgtgggtgag tatgtgtggg gcacaggctg gctccctcag ctcccacgtc 1100  
ctagaggggg tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150  
goggctgcag tccttttctc cctcaaaggc ctccgaccct cagctggagg 1200  
cgggcatctt tcctaaaggg tccccatagg gtctggttcc accccatccc 1250  
aggtctgtgg tcagagcctg ggagggttcc ctacgatggt taggggtgcc 1300  
ccatggaggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350  
tgaggtaagg ccgccctgac ctggacttca gggggagggg gtaaaggag 1400  
agaggagggg ggctagggg tcctctagat cagtgggggc actgcagggtg 1450  
gggctctccc tatacctggg acacctgctg gatgtcacct ctgcaaccac 1500  
acccatgtgg tggtttcatg aacagaccac gtcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
 ggccctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700  
 cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750  
 gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800  
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttgccc 1850  
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
 gctgggcctg ccccagggca acgtgggggc ggagactcag ctggacagcc 1950  
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
     1                    5                    10                    15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
                     20                    25                    30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
                     35                    40                    45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
                     50                    55                    60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
                     65                    70                    75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
                     80                    85                    90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
                     95                    100                    105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
                     110                    115                    120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
                     125                    130                    135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro





Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	
				200					205					210	
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr	
				215					220					225	
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	
				230					235					240	
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly	
				245					250					255	
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys	
				260					265					270	

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 359  
 ccagcagtgc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
ccggcgcggg tggcggagag atcagaagcc tcttcccaa gccgagccaa 100  
cctcagcggg gaccgggct cagggacgcg gcggcggcgg cggcgactgc 150  
agtggctgga cgatggcagc gtccgcggga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcggcg gcgcttgggc 250  
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcggttga cctcagtctc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actccaagg gcaagtgtac 450  
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
cctggacaca ttaggtctta tgctgtagaa aaagagaatt tgctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850  
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900  
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
 atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100  
 ggagagaaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
 cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200  
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
 tgccttaatg gagacaatag cagatcctgt agtattttcca gtagacatgg 1350  
 ccttttaatc taagggtcta agactgatta gtcttagcat ttactgtagt 1400  
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450  
 cagtatcagt accattttatt tgtctgccgc ttttaaaaaa taccattgg 1500  
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
 attagcaaag gataaatgcc gaagggtcact tcattctgga cacagttgga 1700  
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<400> 364  
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
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 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
 20 25 30  
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
 35 40 45  
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
 50 55 60  
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
 65 70 75  
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
 80 85 90  
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
 95 100 105



Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
				260					265					

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50  
 cgggctgccc cccccggggg cttggcctca agctgcggac gacgcggggg 100  
 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150  
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
 aggggcgcgg ccccggcgca gtcccccgcg gccccgacc ctgaggcgctc 250  
 gcctctggcc gagcggccac aggagcagtc cctcgccccg tggctctccgc 300  
 agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350  
 agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcat 400  
 agtggttga gtttctgtag atggaaaaga agtctgtgta gaaggtttag 450  
 gttatgctga tgttgagaac cgtgtacat gtaaaccaga gacagttatg 500

cgaattgcta	gcatcagcaa	aagtctcacc	atggttgctc	ttgccaaatt	550
gtgggaagca	gggaaactgg	atcttgatat	tccagtacaa	cattatgttc	600
ccgaattccc	agaaaaagaa	tatgaagggtg	aaaagggttc	tgtcacaaca	650
agattactga	tttcccattt	aagtggaatt	cgtcattatg	aaaaggacat	700
aaaaaagggtg	aaagaagaga	aagcttataa	agccttgaag	atgatgaaag	750
agaatgttgc	atttgagcaa	gaaaaagaag	gcaaaagtaa	tgaaaagaat	800
gattttacta	aatttaaaac	agagcaggag	aatgaagcca	aatgccggaa	850
ttcaaaacct	ggcaagaaaa	agaatgattt	tgaacaaggc	gaattatatt	900
tgagagaaaa	gtttgaaaat	tcaattgaat	ccctaagatt	atttaaaaaat	950
gatcctttgt	tcttcaaacc	tggtagtcag	tttttgtatt	caacttttgg	1000
ctatacccta	ctggcagcca	tagtagagag	agcttcagga	tgtaaataatt	1050
tggactatat	gcagaaaata	ttccatgact	tggatatgct	gacgactgtg	1100
caggaagaaa	acgagccagt	gattttacaat	agagcaagggt	aaatgaatac	1150
cttctgctgt	gtctagctat	atcgcatctt	aacactatct	tattaattaa	1200
aagtcaaatt	ttctttgttt	ccattccaaa	atcaacctgc	cacatttttg	1250
gagcttttct	acatgtctgt	tttctcatct	gtaaagtgaa	ggaagtaaaa	1300
catgtttata	aagtaaaaaa	a	1321		

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<210> 366
<211> 373
<212> PRT
<213> Homo sapiens
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<400> 366
Met  Tyr  Arg  Leu  Leu  Ser  Ala  Val  Thr  Ala  Arg  Ala  Ala  Ala  Pro
  1      5      10      15

Gly  Gly  Leu  Ala  Ser  Ser  Cys  Gly  Arg  Arg  Gly  Val  His  Gln  Arg
      20      25      30

Ala  Gly  Leu  Pro  Pro  Leu  Gly  His  Gly  Trp  Val  Gly  Gly  Leu  Gly
      35      40      45

Leu  Gly  Leu  Gly  Leu  Ala  Leu  Gly  Val  Lys  Leu  Ala  Gly  Gly  Leu
      50      55      60

Arg  Gly  Ala  Ala  Pro  Ala  Gln  Ser  Pro  Ala  Ala  Pro  Asp  Pro  Glu
      65      70      75

Ala  Ser  Pro  Leu  Ala  Glu  Pro  Pro  Gln  Glu  Gln  Ser  Leu  Ala  Pro
      80      85      90

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Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370	

<210> 367

<211> 30  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-30  
<223> Synthetic construct.

<400> 367  
tggaaaagaa gtctggtcag aaggttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggtt cattctcctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
aaaacctcag aacaactcat ttgcacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50



Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373  
 <211> 1706  
 <212> DNA  
 <213> Homo sapiens

<400> 373  
 ggagcgtctgc tggaacccga gccggagccg gagccacagc ggggaggggtg 50  
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100  
 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150  
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc	tggaagggcc	tgcagcaatc	cctccttcct	tcggtttcaa	250
ctggacttct	atcaggtcta	cttcctggcc	ctggcagctg	attggcttca	300
ggccccctac	ctctataaac	tctaccagca	ttactacttc	ctggaaggtc	350
aaattgccat	cctctatgtc	tgtggccttg	cctctacagt	cctctttggc	400
ctagtggcct	cctcccttgt	ggattggctg	ggtcgcaaga	attcttgtgt	450
cctctttctc	ctgacttact	cactatgctg	cttaaccaa	ctctctcaag	500
actactttgt	gctgctagt	gggcgagcac	ttggtgggct	gtccacagcc	550
ctgctcttct	cagccttcga	ggcctgggat	atccatgagc	acgtggaacg	600
gcatgacttc	cctgctgagt	ggatcccagc	tacctttgct	cgagctgcct	650
tctggaacca	tgtgctggct	gtagtggcag	gtgtggcagc	tgaggctgta	700
gccagctgga	tagggctggg	gcctgtagcg	ccctttgtgg	ctgccatccc	750
tctcctggct	ctggcagggg	ccttggccct	tcgaaactgg	ggggagaact	800
atgaccggca	gcgtgccttc	tcaaggacct	gtgctggagg	cctgcgctgc	850
ctcctgtcgg	accgccgcgt	gctgctgctg	ggcaccatac	aagctctatt	900
tgagagtgtc	atcttcatct	ttgtcttcct	ctggacacct	gtgctggacc	950
cacacggggc	ccctctgggc	attatcttct	ccagcttcat	ggcagccagc	1000
ctgcttggct	cttccttgta	ccgtatcgcc	acctccaaga	ggtaccacct	1050
tcagcccatg	cacctgctgt	cccttgctgt	gctcatcgtc	gtcttctctc	1100
tcttcatgtt	gactttctct	accagcccag	gccaggagag	tccggtggag	1150
tccttcatag	cctttctact	tattgagttg	gcttgtggat	tatactttcc	1200
cagcatgagc	ttcctacgga	gaaagggtgat	ccctgagaca	gagcaggctg	1250
gtgtactcaa	ctggttccgg	gtacctctgc	actcactggc	ttgcctaggg	1300
ctccttgtcc	tccatgacag	tgatcgaaaa	acaggcactc	ggaatatgtt	1350
cagcatttgc	tctgctgtca	tggatgatggc	tctgctggca	gtggtgggac	1400
tcttcaccgt	ggtaaggcat	gatgctgagc	tgcggttacc	ttcacctact	1450
gaggagccct	atgcccctga	gctgtaacct	cactccagga	caagatagct	1500
gggacagact	cttgaattcc	agctatccgg	gattgtacag	atctctctgt	1550
gactgacttt	gtgactgtcc	tgtggtttct	cctgccattg	ctttgtgttt	1600
gggaggacat	gatgggggtg	atggactgga	aagaagggtgc	caaaagttcc	1650

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700  
aaaaaa 1706

<210> 374  
<211> 450  
<212> PRT  
<213> Homo sapiens

<400> 374  
Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser  
1 5 10 15  
Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly  
20 25 30  
Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe  
35 40 45  
Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala  
50 55 60  
Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly  
65 70 75  
Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu  
80 85 90  
Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys  
95 100 105  
Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu  
110 115 120  
Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala  
125 130 135  
Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala  
140 145 150  
Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu  
155 160 165  
Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val  
170 175 180  
Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp  
185 190 195  
Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu  
200 205 210  
Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn  
215 220 225  
Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu  
230 235 240





ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350  
ctctccaaga ctcggtggtt ccaggagcac ggcgggcggg cggatgatcat 400  
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
acagtacca ggcacagct gacatccccg ccctcttctt gctcggccga 500  
gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600  
tgcaaccgcc ctggaccttc tggtagaaga gtttgtocca cattccagcc 650  
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
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cccaggggcc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
ccccagggtt tctggctaga acccgaaaca aaaggagctg aaggcagggtg 900  
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050  
taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376  
<211> 188  
<212> PRT  
<213> Homo sapiens

<400> 376  
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu  
1 5 10 15  
Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu  
20 25 30  
Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr  
35 40 45  
Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr  
50 55 60  
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly  
65 70 75  
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val  
80 85 90

Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccagc ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50  
ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100  
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgctc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450  
tttggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500  
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650  
ggatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1					5				10				15	
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20				25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
			35					40					45	

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
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 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100  
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt ttttctctggg 400  
 tgtcagcgag ccctgactca ctacagtgcg gctgacaggg gctgtcatgc 450  
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550  
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650



ttgaactctg gtgactatca agggaacgcy atgccccccc tccccctccc 2150  
 tctccctctc acttttggtg caagatcctt ccttgtccgt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataaccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385  
 <211> 513  
 <212> PRT  
 <213> Homo sapiens

<400> 385  
 Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala  
 1 5 10 15  
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala  
 20 25 30  
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val  
 35 40 45  
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser  
 50 55 60  
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys  
 65 70 75  
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu  
 80 85 90  
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe  
 95 100 105  
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg  
 110 115 120  
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu  
 125 130 135  
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser  
 140 145 150  
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg  
 155 160 165  
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys  
 170 175 180  
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser  
 185 190 195  
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu



				200					205					210
His	Leu	Glu	His	Asn 215	Gln	Phe	Ser	Lys	Leu 220	Asn	Leu	Ala	Leu	Phe 225
Pro	Arg	Leu	Val	Ser 230	Leu	Gln	Asn	Leu	Tyr 235	Leu	Gln	Trp	Asn	Lys 240
Ile	Ser	Val	Ile	Gly 245	Gln	Thr	Met	Ser	Trp 250	Thr	Trp	Ser	Ser	Leu 255
Gln	Arg	Leu	Asp	Leu 260	Ser	Gly	Asn	Glu	Ile 265	Glu	Ala	Phe	Ser	Gly 270
Pro	Ser	Val	Phe	Gln 275	Cys	Val	Pro	Asn	Leu 280	Gln	Arg	Leu	Asn	Leu 285
Asp	Ser	Asn	Lys	Leu 290	Thr	Phe	Ile	Gly	Gln 295	Glu	Ile	Leu	Asp	Ser 300
Trp	Ile	Ser	Leu	Asn 305	Asp	Ile	Ser	Leu	Ala 310	Gly	Asn	Ile	Trp	Glu 315
Cys	Ser	Arg	Asn	Ile 320	Cys	Ser	Leu	Val	Asn 325	Trp	Leu	Lys	Ser	Phe 330
Lys	Gly	Leu	Arg	Glu 335	Asn	Thr	Ile	Ile	Cys 340	Ala	Ser	Pro	Lys	Glu 345
Leu	Gln	Gly	Val	Asn 350	Val	Ile	Asp	Ala	Val 355	Lys	Asn	Tyr	Ser	Ile 360
Cys	Gly	Lys	Ser	Thr 365	Thr	Glu	Arg	Phe	Asp 370	Leu	Ala	Arg	Ala	Leu 375
Pro	Lys	Pro	Thr	Phe 380	Lys	Pro	Lys	Leu	Pro 385	Arg	Pro	Lys	His	Glu 390
Ser	Lys	Pro	Pro	Leu 395	Pro	Pro	Thr	Val	Gly 400	Ala	Thr	Glu	Pro	Gly 405
Pro	Glu	Thr	Asp	Ala 410	Asp	Ala	Glu	His	Ile 415	Ser	Phe	His	Lys	Ile 420
Ile	Ala	Gly	Ser	Val 425	Ala	Leu	Phe	Leu	Ser 430	Val	Leu	Val	Ile	Leu 435
Leu	Val	Ile	Tyr	Val 440	Ser	Trp	Lys	Arg	Tyr 445	Pro	Ala	Ser	Met	Lys 450
Gln	Leu	Gln	Gln	Arg 455	Ser	Leu	Met	Arg	Arg 460	His	Arg	Lys	Lys	Lys 465
Arg	Gln	Ser	Leu	Lys 470	Gln	Met	Thr	Pro	Ser 475	Thr	Gln	Glu	Phe	Tyr 480
Val	Asp	Tyr	Lys	Pro 485	Thr	Asn	Thr	Glu	Thr 490	Ser	Glu	Met	Leu	Leu 495

365

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 386  
 ctgggatctg aacagtttcg gggc 24

<210> 387  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 387  
 ggtccccagg acatggtctg tccc 24

<210> 388  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 388  
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
 <211> 1449  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100  
 gogatotcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
 ctcggaccta coatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tctgctgct ggTTTTggtg 250  
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300  
 gagaccccgga attgattctc acaggcgcac catggcagtt tttgctgttg 350  
 gagacttggga ctctatTTtat gggacagaag cagctgtgag tccaactgtt 400  
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttcctgctcc 450  
 atgTTTTggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500  
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550  
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
 tccagagatc tattcatata gtctgaggaa ggacaattcg aaaaaagaat 650  
 ggatgttggga aaaaattttg gtcattggaga tgtttaaata gtaaagtagc 700  
 aggtttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800  
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850  
 tctgctttta actctttcct agcatgggtt ccataaaaat tattataatt 900  
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950  
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
 gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100  
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
 ccaacacggg gagaaaagaa aatttcccct tttacagtaa tgaatgtggc 1200  
 ctccatagtc catagtgttt ctctggagcc tcagggttg gcatttattg 1250  
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400  
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 390  
 Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr  
 1 5 10 15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 391  
 cttttcagtgcacctcagc gatctc 26

<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 392  
 ccaaaacatg gagcaggaac agg 23

<210> 393  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 394  
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50  
accacccggc gtttctccag ctcgatctgg aggetgcttc gccagtgtgg 100  
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt ttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttggga ctcatittggg 500  
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750  
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800  
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850  
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agaaaagctt tataattgct ggcttaggac agagcaatac ttacaataa 950  
aagctctaca ctttttcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100



Leu	Leu	Leu	Leu	Val	Phe	Gly	Leu	Ile	Trp	Gly	Leu	Met	Leu	Leu
				20					25					30
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35					40					45
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50					55					60
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65					70					75
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80					85					90
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95					100					105
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110					115					120
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125					130					135
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396  
 <211> 2639  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
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 gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150  
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcatc tcaccactg ctttctcccg cttcgtctac ctggagtcgc 400  
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
 agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500  
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
 acctctccca caacctcatt caccgcctcg tgccccaccc cagcagggcc 600  
 ggctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg	cccaacctcc	gagacttgcc	cctgcgctac	ctgagcctgg	700
atgggaaccc	tctagctgtc	attgggtccg	gtgccttcgc	ggggctggga	750
ggccttacac	acctgtctct	ggccagcctg	cagaggctcc	ctgagctggc	800
gcccagtggc	ttccgtgagc	taccgggcct	gcaggctcctg	gacctgtcgg	850
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ggcgctgctc	ctccacctcc	cggcactgca	gagcgtcagc	gtggggccagg	1000
atgtgcggtg	ccggcgccctg	gtgcggggagg	gcacctaccc	ccggaggcct	1050
ggctccagcc	ccaagggtgcc	cctgcactgc	gtagacaccc	gggaatctgc	1100
tgccaggggc	cccaccatct	tgtgacaaat	ggtgtggccc	agggccacat	1150
aacagactgc	tgtcctgggc	tgctcaggt	cccagtaac	ttatgttcaa	1200
tgtgccaaca	ccagtgggga	gcccgcaggc	ctatgtggca	gcgtcaccac	1250
aggagttgtg	ggcctaggag	aggctttgga	cctgggagcc	acacctagga	1300
gcaaagtctc	acccctttgt	ctacgttgct	tccccaaacc	atgagcagag	1350
ggacttcgat	gccaaaccag	actcgggtcc	cctcctgctt	cccttcccca	1400
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tcttttctaa	catagccctt	tctttgccat	gaggccatga	ggcccgcctt	1600
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gcctcctgcc	tcccagccc	gacccaatgc	actttcttgt	ctcctcta	1800
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cattagcaca	ggagtagcag	cagcaggaca	ggcaagagcc	tcacaagtgg	1900
gactctgggc	ctctgaccag	ctgtgcggca	tgggctaagt	cactctgccc	1950
ttcggagcct	ctggaagctt	agggcacatt	ggttccagcc	tagccagttt	2000
ctcacccctg	gttggggctc	cccagcatcc	agactggaaa	cctaccatt	2050
ttcccctgag	catcctctag	atgctgcccc	aaggagttgc	tgcagttctg	2100





Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser
	155	160 165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly
	170	175 180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg
	185	190 195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu
	200	205 210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe
	215	220 225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln
	230	235 240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly
	245	250 255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala
	260	265 270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp
	275	280 285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu
	290	295 300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg
	305	310 315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly
	320	325 330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser
	335	340 345
Ala Ala Arg Gly	Pro Thr Ile Leu	
	350	

<210> 398  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 398  
 ccctgccagc cgagagcttc acc 23

<210> 399  
 <211> 23  
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150  
atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200  
ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250  
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300  
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ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550  
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402  
<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 402  
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Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu  
20 25 30  
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys  
35 40 45  
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
50 55 60  
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu  
65 70 75  
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser  
80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
				95					100					105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
				110					115					120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
				125					130					135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
				140					145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
				155					160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
				170					175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
				185					190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
				200					205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
				215					220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
				230					235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
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Trp	Met	Glu	Glu	Thr	Glu									
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<210> 403  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 403  
 ctccctgtggt ctccagattt caggccta 28

<210> 404  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgccat ttacagacac gtagtgatt ctggaggtcg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtc tggagggat gatggctggg gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
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gctgggtacc caatatacaa agagcagcac tggatgaat gggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcag gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggatgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttctgg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala		20	25	30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr		35	40	45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp		50	55	60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala		65	70	75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly		80	85	90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg		95	100	105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser		110	115	120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met		125	130	135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu		140	145	150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly		155	160	165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile		170	175	180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro		185	190	195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr		200	205	210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu		215	220	225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu		230	235	240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg		245	250	255
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr		260	265	270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly		275	280	285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met		290	295	300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg				









<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414  
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100  
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcctc 350  
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
catgaaaacc atccgtctgc cacgctggct ggagcctcg cccaccaagg 450  
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500  
aactactttg cgttttaaat ctgcagtggg gccgccaacg tcgtgggccc 550  
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600  
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650  
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700  
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750  
acgacgatcc agggacccaa atgaacgatg aaagcaggaa actcttctct 800  
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850  
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900  
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000  
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050  
cccggcaggg gctgaggagg aggagcaggg ggtgctgctg ggaaggtgct 1100  
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337



<222> 1-21  
<223> Synthetic construct.

<400> 416  
gccatagtca cgacatggat g 21

<210> 417  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 417  
ggatggccag agctgctg 18

<210> 418  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 418  
aaagtacaag tgtggcctca tcaagc 26

<210> 419  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 419  
tctgactcct aagtcaggca ggag 24

<210> 420  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 420  
attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200  
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtccct 250  
gcaccccttc ctgggacact atgttggttct ccgccctcct gctggaggtg 300  
atgttgatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctgagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850







<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 424  
gtaaagtcgc tggccagc 18

<210> 425  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 425  
cccgatctgc ctgctgta 18

<210> 426  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 426  
ctgcactgta tggccattat tgtg 24

<210> 427  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 427  
cagaaacca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428  
<211> 1073  
<212> DNA  
<213> Homo sapiens

<400> 428  
aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
acattttgcc tctgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct ccacaaaaac tggtccgga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaata 300  
 ctgctgcagg aatgacacct ggtaccaga cccacccatt gaccctggga 350  
 gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcacctg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850  
 gaaaatatcc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgctgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg  
 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430  
 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

<400> 430  
 ggagagaggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50  
 cggagcgcgg cggagccaga cgtgaccac gttcctctcc tcggtctcct 100  
 ccgcctccag ctccgcgctg ccgggcagcc gggagccatg cgaccccagg 150  
 gccccgcgcg ctccccgcag cggctccgcg gcctcctgct gctcctgctg 200  
 ctgcagctgc ccgcgccgtc gagcgccctct gagatcccca aggggaagca 250  
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctgggtc gagacgggag cctgggggcc 350  
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600  
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttatTTT ggaccaagga agccctgaaa tgaattcaac 700  
aattaatatt catcgcaatt cttctgtgga aggactttgt gaaggaattg 750  
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcaacttaaat gacatttttaa ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
tgatttcaca ctgttttttaa atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
aatttgtaaa tgtaagaat tttttttata tctgttaaatt aaaaattatt 1250  
tccaaca 1257

<210> 431  
<211> 243  
<212> PRT  
<213> Homo Sapien

<400> 431  
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
1 5 10 15  
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
20 25 30  
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
35 40 45  
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
50 55 60  
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
65 70 75  
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
80 85 90  
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
95 100 105  
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
110 115 120  
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial Sequence

<400> 432  
 aggacttgcc ctcaggaa 18

<210> 433  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 cgcaggacag ttgtgaaaat a 21

<210> 434  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 435  
 cccacctgta ccaccatgt 19  
  
 <210> 436  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 436  
 actccaggca ccattctgttc tccc 24  
  
 <210> 437  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 437  
 aagggtggc attcaagtc 19  
  
 <210> 438  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 438  
 tgacctggca aaggaagaa 19  
  
 <210> 439  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 439  
 cagccaccct ccagtccaag g 21  
  
 <210> 440  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtgtt ttggagaga 19

<210> 441  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gagcaccaat 20

<210> 442  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttaaagtcc aaga 24

<210> 444  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 445  
 agcgtacact ctctccaggc aaccag 26  
  
 <210> 446  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 446  
 caattctgga tgaggtgga ga 22  
  
 <210> 447  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 447  
 caggactgag cgcttggtta 20  
  
 <210> 448  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 448  
 caaagcgcca agtaccggac c 21  
  
 <210> 449  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 449  
 ccagacctca gccaggaa 18  
  
 <210> 450  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 450  
 ccctagctga ccccttca 18



<210> 451  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 451  
tctgacaagc agttttctga atc 23

<210> 452  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 452  
ctctccccct cccttttctt ttgttt 26

<210> 453  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 453  
ctctggtgcc cacagtga 18

<210> 454  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 454  
ccatgcctgc tcagccaaga a 21

<210> 455  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 455  
caggaaatct ggaaacctac agt 23

<210> 456  
<211> 20  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gaccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacaccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461  
tggacacgtg gcagtgga 18

<210> 462  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
tcatggtctc gtccattc 19

<210> 463  
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